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(54) Title: CELL LINES AND HOST NUCLEIC ACID SEQUENCES RELATED TO INFECTIOUS DISEASE

(57) Abstract: Host nucleic acids and host proteins that participate in viral infection, such as human immunodeficiency virus (HIV), influenza A, and Ebola virus, have been identified. Interfering with or disrupting the interaction between a host nucleic acid or host protein and a virus or viral protein confers an inhibition of or resistance to infection. Thus, interfering with such an interaction in a host subject can confer a therapeutic or prophylactic effect against a virus. The sequences identified can be used to identify agents that reduce or inhibit viral infection.

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## CELL LINES AND HOST NUCLEIC ACID SEQUENCES RELATED TO INFECTIOUS DISEASE

### CROSS REFERENCE TO RELATED APPLICATIONS

5 This application claims the benefit of U.S. Provisional Application Nos. 60/427,464 filed November 18, 2002 and 60/482,604 filed June 25, 2003, both herein incorporated by reference.

### FIELD

10 The present disclosure relates to host nucleic acid sequences, and proteins encoded by these sequences, that are involved in viral infection or are otherwise associated with the life cycle of a virus. Decreasing or inhibiting the interaction of these host sequences with a viral sequence can be used to decrease or inhibit infection by the virus.

### BACKGROUND

15 Infectious diseases affect the health of people and animals around the world, causing serious illness and death. Public health efforts have focused on behavioral modification and other public health efforts to reduce the incidences of infection, while treatment regimens for these diseases have focused on pharmaceuticals, such as antibiotics and anti-viral medications. However, educating people about modifying behavior can be difficult, and that approach alone rarely can significantly  
20 diminish the incidence of infection. Furthermore, modifying the behavior of domestic or wild animals would not result in diminished infections. Stopping the spread of infections in an animal population typically involves wholesale slaughter. Few vaccines are available or wholly effective, and they tend to be specific for particular conditions.

25 The rate of HIV (human immunodeficiency virus) infection is increasing. HIV and its associated acquired immune deficiency syndrome (AIDS) accounted for approximately 5% of all deaths in the United States in the year 2000, while over 313,000 persons were reported to be living with AIDS in that same year. Centers for Disease Control and Prevention, *HIV/AIDS Surveillance Supplemental Report*, 8(1):1-22 (2002). These increasing infection rates have occurred, even though the mode of HIV infection has been known for almost 20 years, and educational programs around the  
30 world have promoted behavioral modifications meant to reduce HIV infection. Incidence and death rates due to HIV disease have been decreasing since the mid-90's, in part due to aggressive antiviral therapies, which frequently have toxic side effects and strict dosage schedules. However, even with treatment, the patient is not cured of the disease, and to date, no effective vaccine therapy has been found.

35 In other diseases, such as infection by the Ebola virus, not only are treatments limited, but containment or prevention of infections is difficult because the life cycle of the virus is not well known. The natural reservoir for the Ebola virus, that is the place or population in nature where the virus resides between human outbreaks, has not yet been identified.

Additionally, different viral strains can rapidly evolve in response to drug usage, producing drug-resistant strains. For example, strains of the influenza virus resistant to amantadine and rimantadine have recently arisen. A recent study of 80 newly-infected people conducted by the AIDS Research Center at Rockefeller University in New York, found that as many as 16.3% of these individuals had strains of HIV associated with resistance to some treatments, and 3.8% appeared to be resistant to several currently available anti-HIV drugs. Thus, a need exists for alternative treatments for infectious disease and methods of designing new drugs to combat infectious disease.

### SUMMARY

Several host nucleic acid sequences involved in viral infection have been identified using gene trap methods. The identification of these host sequences and their encoded products permits the identification of sequences that can be targeted for therapeutic intervention.

The disclosed host sequences (including the target sequences associated with SEQ ID NOS: 1-227, 229, and 231, and the proteins encoded thereby (such as SEQ ID NOS: 228, 230, and 232), as well as variants, fusions, and fragments thereof that retain the appropriate biological activity) can mediate infection, and in some examples these host nucleic acids are required for infection. For example, the host nucleic acid can encode a cellular receptor or ligand or a fragment thereof that is recognized by a virus, such as the T-cell V-D-J beta 2.1 chain. In another example, the host nucleic acid encodes an enzyme that mediates viral infection, such as the  $\beta$ -chimerin rho-GTPase (referred to herein as  $\beta$ -chimerin). In another example, the host nucleic acid encodes a Ras oncogene family member such as Rab9. It is demonstrated herein that Rab9 is a host protein involved in infection by pathogens (such as viruses and bacteria) that use similar pathways for morphogenesis of infectious particles. In particular examples, Rab9 is involved in infection by pathogens (such as viruses and bacteria) that utilize lipid rafts. Thus, for example, interfering with the interaction between the disclosed host proteins and a viral or pathogen protein, for example by disrupting the expression of the host nucleic acid within a host cell, or by administering an agent that decreases binding between a host protein and a viral protein, can inhibit, or even prevent, infection of that host cell by the associated virus. Moreover, the identification of particular host enzymes or other host proteins involved in infection provides a method for developing new therapies targeted at inhibiting infection, at the protein or nucleic acid level.

In some examples, the nucleic acid itself mediates viral infection. For example, the nucleotide sequence of a host nucleic acid in the host genome can be recognized by the virus during integration of the viral genome into the host genome. The identification of nucleic acid sequences that are involved in the pathogenesis of infection therefore provides an important tool for interfering with infection.

This genomics-based discovery of nucleic acids and proteins involved in, or even required for, infection provides a new paradigm for identifying and validating various aspects of infectious disease, including assessing individual or population resistance to infection and finding novel

diagnostic and drug targets for infectious disease and altering the nucleotide sequence of the host nucleic acid.

Based on the identification of several host nucleic acid and protein sequences involved in viral infection, provided herein are methods for decreasing infection of a host cell by a virus, such as HIV, Ebola, or influenza A, or treating such a viral infection, by interfering with the activity or expression of one or more host proteins shown in Table 1 (including the target sequences associated with any of SEQ ID NOS: 1-232, as well as variants, fragments, and fusions thereof), such as at least two host proteins, or at least three host proteins. Also provided are methods for identifying agents that can decrease viral infection of a host cell, such as infection by HIV, Ebola, or influenza A. In addition, cells and non-human mammals are provided that have decreased susceptibility to viral infection, such as HIV, Ebola, or influenza A infection.

### BRIEF DESCRIPTION OF THE FIGURES

FIG. 1 is a schematic illustration of the U3neoSV1 retroviral vector, which is capable of isolating the nucleic acids described herein using the gene-trap method.

FIG. 2 is a schematic illustration of the gene-trap method.

FIG. 3 is a schematic illustration of one method of identifying host genes described herein.

FIG. 4 is a flow chart illustrating a method for isolating cells resistant to HIV infection, including HIV-1 and HIV-2 infection.

FIG. 5 is a bar graph showing the relative amount of p24 in HIV-infected cells in the presence of various siRNAs. CHN ( $\beta$ -chimerin); KOX (similar to KOX4 (LOC131880) and LOC166140); RBB (retinoblastoma binding protein 1); RAB (Rab9); KIAA1259; F3 (tissue factor 3; thromboplastin); AXL (AXL receptor tyrosine kinase); Msleb (mammalian selenium binding protein).

FIG. 6 is a schematic drawing showing a model of Rab9 involvement in lipid raft formation.

### SEQUENCE LISTING

The nucleotide sequences of the nucleic acids described herein are shown using standard letter abbreviations for nucleotide bases, and three letter code for amino acids. Only one strand of each nucleic acid sequence is shown, but the complementary strand is understood as included by any reference to the displayed strand. Additionally, the nucleic acid sequences shown in SEQ ID NOS: 1-226 inherently disclose the corresponding polypeptide sequences of coding sequences (resulting translations of the nucleotide sequences), even when those polypeptide sequences are not explicitly provided herein.

SEQ ID NO: 1 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 18E8, entire insert. The human homolog is the (-) strand of GenBank Accession No. NG\_001333.1, T-cell receptor V beta chain (T-cell receptor beta). Further information on the T-cell receptor V beta chain can be found in WO 01/23409, WO 01/55302, WO 01/57182, and WO 01/94629.



SEQ ID NO: 2 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 18BA, distal end. The human homolog is the (-) strand of GenBank Accession No. AC104597.3, T-cell receptor V beta chain.

5 SEQ ID NO: 3 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 18BA, proximal end. The human homolog is the (+) strand of GenBank Accession No. NG\_001333.1, T-cell receptor beta.

SEQ ID NO: 4 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 18BE, distal end. The human homolog is the (+) strand of GenBank Accession No. AC00616.7, T-cell receptor beta.

10 SEQ ID NO: 5 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 18BE, middle of insert. The human homolog is the (-) strand of GenBank Accession No. AC104597.3, T-cell receptor beta.

SEQ ID NO: 6 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 18BE, proximal end. The human homolog is the (+) strand of GenBank Accession No. NG\_001333.1, T-cell receptor beta.

15 SEQ ID NO: 7 is a nucleic acid sequence associated with viral, such as HIV, infection which corresponds to the sequence identified as Nucleotide Sequence 18E6, proximal end. The human homolog is the (-) strand of GenBank Accession No. NG\_001333.1, T-cell receptor beta.

SEQ ID NO: 8 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E21, proximal end. The human homolog is the (+) strand of GenBank Accession No. NG\_001333.1, T-cell receptor beta.

20 SEQ ID NO: 9 is a nucleic acid sequence associated with viral, such as HIV, infection which corresponds to the sequence identified as Nucleotide Sequence 2E22, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC099395.2, T-cell receptor beta.

25 SEQ ID NO: 10 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2B13, proximal end. The human homolog is the (-) strand of GenBank Accession No. NG\_001333.1, T-cell receptor beta.

SEQ ID NO: 11 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2B14, proximal end. The human homolog is the (-) strand of GenBank Accession No. NG\_001333.1, T-cell receptor beta.

30 SEQ ID NO: 12 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2B15, distal end. The human homolog is the (+) strand of GenBank Accession No. NG\_001333.1, T-cell receptor beta.

SEQ ID NO: 13 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2B15, proximal end. The human homolog is the (-) strand of GenBank Accession No. NG\_001333.1, T-cell receptor beta.

35 SEQ ID NO: 14 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2B16, proximal end. The human homolog is the (-) strand of GenBank Accession No. NG\_001333.1, T-cell receptor beta.

SEQ ID NO: 15 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E23, distal end. The human homolog is the (-) strand of GenBank Accession No. NG\_001333.1, T-cell receptor beta.

5 SEQ ID NO: 16 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E23, proximal end. The human homolog is the (+) strand of GenBank Accession No. NG\_001333.1, T-cell receptor beta.

SEQ ID NO: 17 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E24, proximal end. The human homolog is the (+) strand of GenBank Accession No. NG\_001333.1, T-cell receptor beta.

10 SEQ ID NO: 18 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E25, proximal end. The human homolog is the (+) strand of GenBank Accession No. NG\_001333.1, T-cell receptor beta.

SEQ ID NO: 19 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E26, proximal end. The human homolog is the (+) strand of GenBank Accession No. NG\_001333.1, T-cell receptor beta.

15 SEQ ID NO: 20 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 18BD, proximal end. The human homolog is the (+) strand of GenBank Accession No. M16834.1, T-cell receptor V-D-J-beta 2.1 chain (described in WO 02/057414 and Reynolds *et al.*, *Cell* 50(1):107-17, 1987).

20 SEQ ID NO: 21 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 18E7, distal end. The human homolog is the (-) strand of GenBank Accession No. AC004593.1 including beta-chimaerin rho GTPase (CHN2) (for example see WO 01/12659).

25 SEQ ID NO: 22 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 18E7, proximal end. The human homologs are the (-) strand of GenBank Accession No. NG\_001333.1, T-cell receptor beta; and the (+) strand of GenBank Accession No. AC004593.1 including beta-chimaerin (CHN2).

30 SEQ ID NO: 23 is a nucleic acid sequence associated with viral, such as HIV and influenza A, infection, and is the clone identified as Nucleotide Sequence 18E6, distal end. The human homolog is the (+) strand of GenBank Accession No. AL049699.8, including malic enzyme 1 (ME1) NADP(+)-dependent cytosolic. Further information on this gene can be found in WO 01/55301 and WO 01/53312.

35 SEQ ID NO: 24 is a nucleic acid sequence associated with viral, such as HIV and influenza A, infection, and is the clone identified as Nucleotide Sequence 18BD, distal end. The human homolog is the (+) strand of GenBank Accession No. AC123903.1, including hypothetical protein XP\_174419.

SEQ ID NO: 25 is a nucleic acid sequence associated with viral, such as HIV and influenza A, infection, and is the clone identified as Nucleotide Sequence 18E9, distal end. The human

SEQ ID NO: 26 is a nucleic acid sequence associated with viral, such as HIV and influenza A, infection, and is the clone identified as Nucleotide Sequence 18E9, middle of insert. The human homolog is the (+) strand of GenBank Accession No. AC096736.3, a region of chromosome 4q31.3-32.

SEQ ID NO: 27 is a nucleic acid sequence associated with viral, such as HIV and influenza A, infection, and is the clone identified as Nucleotide Sequence 18E9, proximal end. The human homologs are the (-) strand of GenBank Accession No. NG\_001333.1, T-cell receptor beta; and (-) strand of GenBank Accession No. AC096736.3, a region of chromosome 4q31.3-32.

SEQ ID NO: 28 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E21, distal end. The human homolog is the (-) strand of GenBank Accession No. M26920.1, alpha satellite DNA.

SEQ ID NO: 29 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E22, distal end. The human homologs are the (+) strand of GenBank Accession No. AP004369.3, including LOC253788 (and neighboring similar to RIKEN cDNA 1700001L23 (LOC219938)); and the (+) strand of GenBank Accession No. AC093117.2, between coagulation factor III, thromboplastin, tissue factor (F3) and LOC91759.

SEQ ID NO: 30 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2B13, distal end. The human homolog is the (-) strand of GenBank Accession No. AC092043.2, between similar to zinc finger protein 7 KOX4 (LOC131880) and LOC166140.

SEQ ID NO: 31 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2B14, distal end. The human homologs are the (-) strand of GenBank Accession No. AL136963.17, between LOC222474 and similar to Rho guanine nucleotide exchange factor 4, isoform a, APC-stimulated guanine nucleotide exchange factor (LOC221178); and the (+) strand of GenBank Accession No. NG\_001333.1, T-cell receptor beta.

SEQ ID NO: 32 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2B16, distal end. The human homölog is the (-) strand of GenBank Accession No. AL133293.28, between ribosomal protein L7A-like 4 (RPL7AL4) and v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homölog (avian) (SRC).

SEQ ID NO: 33 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E24, distal end. The human homolog is the (-) strand of GenBank Accession No. AL161417.17, KIAA0564.

SEQ ID NO: 34 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E25, distal end. The human homologs are the (-) strand of GenBank Accession No. Z12006.1, alpha satellite DNA; and the (+) and (-) strands of GenBank Accession No. AC093577.2, M96 protein.

SEQ ID NO: 35 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E26, distal end. The human homologs are the (-) strand of GenBank Accession No. Z78022.1, hypothetical protein similar to G proteins, especially RAP-2A (LOC57826); and the (+) strand of GenBank Accession No. AL136220.14, between LOC161005 and osteoblast specific factor 2 (fasciclin I-like; OSF-2).

SEQ ID NO: 36 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B3B1, distal end. The canine homolog is the (+) and (-) strand portions of GenBank Accession No. AJ012166.1, *Canis familiaris* TCTA gene, AMT gene, DAG1 gene, and BSN gene.

SEQ ID NO: 37 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B5B5, distal end. The canine homolog is the (+) and (-) strand portions of GenBank Accession No. AJ012166.1, *Canis familiaris* TCTA gene, AMT gene, DAG1 gene, and BSN gene.

SEQ ID NO: 38 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1B1, distal end. The human homolog is the (+) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

SEQ ID NO: 39 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1B2, distal end. The human homolog is the (-) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

SEQ ID NO: 40 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1B4, distal end. The human homolog is the (-) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

SEQ ID NO: 41 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1B5, distal end. The human homolog is the (-) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

SEQ ID NO: 42 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1B6, distal end. The human homolog is the (-) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

SEQ ID NO: 43 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1E3, entire insert. The human homolog is the (+) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

SEQ ID NO: 44 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1E5, proximal end. The human

homolog is the (-) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

SEQ ID NO: 45 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B6B1, entire insert. The human homolog is the (-) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

SEQ ID NO: 46 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B6E1, distal end. The human homolog is the (+) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

SEQ ID NO: 47 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B6E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

SEQ ID NO: 48 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B6E3, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

SEQ ID NO: 49 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1E1, distal end. The human homolog is the (+) strand of GenBank Accession No. AC104036.8, between LOC253121 and hyaluronan synthase 2 (HAS2).

SEQ ID NO: 50 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. AF260225.1, Testin 2 and Testin 3 (see WO 01/57270, WO 01/57271, WO 01/57273, WO 01/57274, WO 01/57275, WO 01/57276, WO 01/57277, WO 01/57278, or Tatarelli *et al.*, *Genomics* 68(1):1-12, 2000).

SEQ ID NO: 51 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1E4, distal end. The human homolog is the (+) strand of GenBank Accession No. AF260225.1, Testin 2 and Testin 3.

SEQ ID NO: 52 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1E4, proximal end. The human homolog is the (-) strand of GenBank Accession No. AF260225.1, Testin 2 and Testin 3.

SEQ ID NO: 53 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B6E2, distal end. The human homolog is the (+) strand of GenBank Accession No. AF260225.1, Testin 2 and Testin 3.

SEQ ID NO: 54 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B6E2, proximal end. The human homolog is the (-) strand of GenBank Accession No. AF260225.1, Testin 2 and Testin 3.

SEQ ID NO: 55 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B6E4, proximal end. The human homolog is the (-) strand of GenBank Accession No. AF260225.1, Testin 2 and Testin 3.

5 SEQ ID NO: 56 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B7E1, distal end. The human homolog is the (+) strand of GenBank Accession No. AF260225.1, Testin 2 and Testin 3.

SEQ ID NO: 57 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B7E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. AF260225.1, Testin 2 and Testin 3.

10 SEQ ID NO: 58 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B5E2, distal end. The human homolog is the (-) strand of GenBank Accession No. AL133230.25, PTPN1 gene for protein tyrosine phosphatase, non-receptor type 1 (see Watanabe *et al.*, *Jpn. J. Cancer Res.* 93:1114-22, 2002).

15 SEQ ID NO: 59 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B5E2, middle of insert. The human homolog is the (-) strand of GenBank Accession No. AL133230.25, PTPN1 gene for protein tyrosine phosphatase, non-receptor type 1.

20 SEQ ID NO: 60 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B3E11, distal end. The human homolog is the (+) strand of GenBank Accession No. AL445675.9, between LOC149360 and LOC253961.

SEQ ID NO: 61 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B3E11, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL391986.12, between KIAA1560 and Tectorin beta (TECTB).

25 SEQ ID NO: 62 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B6E3, distal end. The human homolog is the (-) strand of GenBank Accession No. AC016826.9, including Cadherin related 23 (CDH23).

30 SEQ ID NO: 63 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B6E4, distal end. The human homolog is the (+) strand of GenBank Accession No. AL357372.12, Myeloid/lymphoma or mixed lineage leukemia, translocated to 10 (MMLT10).

35 SEQ ID NO: 64 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence ZV1-1B5, distal end. The human homolog is the (-) strand of GenBank Accession No. AL355802.13, between exportin 5 (XPO5) and DNA polymerase eta (POLH).

SEQ ID NO: 65 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence ZV1-1B5, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL355802.13, between XPO5 and POLH.

SEQ ID NO: 66 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence ZV1-1E, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL355802.13, between XPO5 and POLH.

5 SEQ ID NO: 67 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2E1, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL135744.4, including heterogenous nuclear riboprotein C (C1/C2) (HNRPC).

10 SEQ ID NO: 68 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2E5, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL135744.4, including HNRPC.

SEQ ID NO: 69 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2E6, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL135744.4, including HNRPC.

15 SEQ ID NO: 70 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2B2, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL135744.4, including HNRPC.

SEQ ID NO: 71 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2B13, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL135744.4, including HNRPC.

20 SEQ ID NO: 72 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2B14, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL135744.4, including HNRPC.

25 SEQ ID NO: 73 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2B21, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL135744.4, including HNRPC.

SEQ ID NO: 74 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2B25, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL135744.4, including HNRPC.

30 SEQ ID NO: 75 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2B35, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL135744.4, including HNRPC.

35 SEQ ID NO: 76 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2E5, distal end. The human homolog is the (+) and (-) strands of GenBank Accession No. AL050324.5, including alpha-endosulfine pseudogene (ENSAP) and LOC128741.

SEQ ID NO: 77 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2E6, distal end. The human homolog is the (+) strand of GenBank Accession No. AC017060.7, including LOC222888.

SEQ ID NO: 78 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2B13, distal end. The human homolog is the (+) strand of GenBank Accession No. AL161731.20, between LOC138421 and zinc finger protein 297B (ZNF297B).

- 5        SEQ ID NO: 79 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2B14, distal end. The human homolog is the (-) strand of GenBank Accession No. AC012366.10, including sideroflexin 5 (SFXN5).

- 10       SEQ ID NO: 80 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2B35, distal end. The human homolog is the (+) strand of GenBank Accession No. AL645504.10, including importin 9 (FLJ10402).

SEQ ID NO: 81 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence GV1-1B1, distal end. The human homolog is the (+) strand of GenBank Accession No. NG\_001333.1, T-cell receptor beta.

- 15       SEQ ID NO: 82 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence GV1-1B1, proximal end. The human homolog is the (+) strand of GenBank Accession No. NG\_001333.1, T-cell receptor beta.

SEQ ID NO: 83 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-B1, distal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

- 20       SEQ ID NO: 84 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E2, distal end. The human homolog is the (+) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

- 25       SEQ ID NO: 85 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E2, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

SEQ ID NO: 86 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E3, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

- 30       SEQ ID NO: 87 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E4, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

SEQ ID NO: 88 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E5, distal end. The human homolog is the (+) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

- 35       SEQ ID NO: 89 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E5, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.



SEQ ID NO: 90 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-B1, distal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

5 SEQ ID NO: 91 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E2, distal end. The human homolog is the (+) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

SEQ ID NO: 92 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E2, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

10 SEQ ID NO: 93 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E4, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

SEQ ID NO: 94 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-B1, distal end. The human homolog is the (+) and (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

15 SEQ ID NO: 95 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-E1, distal end. The human homolog is the (+) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

SEQ ID NO: 96 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

SEQ ID NO: 97 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-E4, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

25 SEQ ID NO: 98 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-E5, distal end. The human homolog is the (+) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

SEQ ID NO: 99 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-E5, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

30 SEQ ID NO: 100 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E1, distal end. The human homolog is the (+) strand of GenBank Accession No. AC021753.7, hypothetical protein KIAA1259.

35 SEQ ID NO: 101 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC021753.7, hypothetical protein KIAA1259.

SEQ ID NO: 102 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E3, distal end. The human homolog is the

(+) and (-) strands of GenBank Accession No. AC107081.5, copper metabolism gene (MURR1) and chaperonin containing TCP1, subunit 4 (CCT4).

SEQ ID NO: 103 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E4, distal end. The human homolog is the (-) strand of GenBank Accession No. AC099785.2, hypothetical protein FLJ40773 and similar to ribosomal protein L24-like (LOC149360).

SEQ ID NO: 104 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E4, distal end. The human homolog is the (+) strand of GenBank Accession No. AF260225.1, Testin 2 and 3 (TES).

SEQ ID NO: 105 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E4, proximal end. The human homolog is the (-) strand of GenBank Accession No. AF260225.1, Testin 2 and 3 (TES).

SEQ ID NO: 106 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E7, distal end. The human homolog is the (+) strand of GenBank Accession No. AF260225.1, Testin 2 and 3 (TES).

SEQ ID NO: 107 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E7, proximal end. The human homolog is the (-) strand of GenBank Accession No. AF260225.1, Testin 2 and 3 (TES).

SEQ ID NO: 108 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-B2, distal end. The human homolog is the (+) and (-) strands of GenBank Accession No. AC105934.2, polybromo 1 (PB1).

SEQ ID NO: 109 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-B4, distal end. The human homolog is the (+) strand of GenBank Accession No. AC022506.38, between DNA damage inducible transcript 3 (DDIT3) and KIAA1887.

SEQ ID NO: 110 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-B5, distal end. The human homolog is the (-) strand of GenBank Accession No. AL157834.12, PDZ and LIM domain 1 (elfin) (PDLIM1).

SEQ ID NO: 111 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E1, distal end. The human homolog is the (+) strand of GenBank Accession No. AL110115.38, LOC284803.

SEQ ID NO: 112 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL110115.38, signal peptide peptidase (HM13) and LOC284803.

SEQ ID NO: 113 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E3, distal end. The human homolog is the (-) strand of GenBank Accession No. AL117341.26, containing PRO0097 and adjacent to FLJ31958.

SEQ ID NO: 114 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E3, proximal end. The human homolog is the (-) strand of GenBank Accession No. AP002076.3, small inducible cytokine E, member 1 (endothelial monocyte-activating) (SCYE1).

5 SEQ ID NO: 115 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E6, distal end. The human homolog is the (+) strand of GenBank Accession No. AP002076.3, containing SCYE1.

10 SEQ ID NO: 116 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E6, proximal end. The human homolog is the (-) strand of GenBank Accession No. AP002076.3, containing SCYE1.

SEQ ID NO: 117 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E4, distal end. The human homolog is the (+) and (-) strands of GenBank Accession No. AC132812.9, between E3 ubiquitin ligase (SMURF2) and hypothetical protein MGC40489.

15 SEQ ID NO: 118 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E5, distal end. The human homolog is the (+) strand of GenBank Accession No. AC079383.17, Ras oncogene family member Rab9.

20 SEQ ID NO: 119 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E5, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC079383.17, Ras oncogene family member Rab9.

SEQ ID NO: 120 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-E2, distal end. The human homolog is the (-) strand of GenBank Accession No. AL132989.5, between PRO1617 and retinoblastoma binding protein 1 (RBBP1).

25 SEQ ID NO: 121 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-E2, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL132989.5, RBBP1.

30 SEQ ID NO: 122 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-E3, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL132989.5, retinoblastoma binding protein 1 (RBBP1).

SEQ ID NO: 123 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-E3, distal end. The human homolog is the (+) and (-) strands of GenBank Accession No. AC096669.1, a region of chromosome 2q12.

35 SEQ ID NO: 124 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-E4, distal end. The human homolog is the (-) strands of GenBank Accession No. AF196968.4, elongation factor for selenoprotein translation (SELB).

SEQ ID NO: 125 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-B1, distal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

5 SEQ ID NO: 126 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-B1, proximal end. The human homolog is the (+) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

SEQ ID NO: 127 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

10 SEQ ID NO: 128 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E1, distal end. The human homolog is the (+) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

SEQ ID NO: 129 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E2, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

15 SEQ ID NO: 130 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E3, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

SEQ ID NO: 131 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E4, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

20 SEQ ID NO: 132 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E5, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

25 SEQ ID NO: 133 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E6, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

SEQ ID NO: 134 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E7, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

30 SEQ ID NO: 135 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E8, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

SEQ ID NO: 136 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E9, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

35 SEQ ID NO: 137 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E10, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

SEQ ID NO: 138 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E2, distal end. The human homolog is the (+) strand of GenBank Accession No. AL031293.1, KIAA1026.

5 SEQ ID NO: 139 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E3, distal end. The human homolog is the (+) strand of GenBank Accession No. AL035587.5, trinucleotide repeat containing 5 (TNRC5).

SEQ ID NO: 140 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E4, distal end. The human homolog is the (-) strand of GenBank Accession No. AC126182.2, homogentisate 1,2-dioxygenase (HGD).

10 SEQ ID NO: 141 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E5, distal end. The human homolog is the (+) strand of GenBank Accession No. AL591643.4, a region of chromosome Xq23-24.

SEQ ID NO: 142 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E6, distal end. The human homolog is the (-) strand of GenBank Accession No. AC113603.3, a region of chromosome 4p15.3.

15 SEQ ID NO: 143 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E7, distal end. The human homolog is the (+) strand of GenBank Accession No. AC011995.8, similar to LWamide neuropeptide precursor protein [Hydractinia echinata] (LOC129883).

20 SEQ ID NO: 144 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E8, distal end. The human homolog is the (-) strand of GenBank Accession No. AC084208.5, a region of chromosome 2q21.

SEQ ID NO: 145 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E9, distal end. The human homolog is the (-) strand of GenBank Accession No. AL391259.15, a region of chromosome Xp11.4, including ubiquitin specific protease 9 (USP9X).

25 SEQ ID NO: 146 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E10, distal end. The human homolog is the (+) strand of GenBank Accession No. AC006397.1, LOC221829.

30 SEQ ID NO: 147 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-B2, distal end. The human homolog is the (+) strand of GenBank Accession No. X14945.1, U3 small nuclear RNA gene.

SEQ ID NO: 148 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-B2, proximal end. The human homolog is the (+) strand of GenBank Accession No. X14945.1, U3 small nuclear RNA gene.

35 SEQ ID NO: 149 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. X14945.1, U3 small nuclear RNA gene.

SEQ ID NO: 150 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-E2, proximal end. The human homolog is the (-) strand of GenBank Accession No. X14945.1, U3 small nuclear RNA gene.

5 SEQ ID NO: 151 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-E2, distal end. The human homolog is the (-) strand of GenBank Accession No. X14945.1, U3 small nuclear RNA gene.

SEQ ID NO: 152 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-E5, proximal end. The human homolog is the (-) strand of GenBank Accession No. X14945.1, U3 small nuclear RNA gene.

10 SEQ ID NO: 153 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV8-E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. X14945.1, U3 small nuclear RNA gene.

SEQ ID NO: 154 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV8-E1, distal end. The human homolog is the  
15 (+) strand of GenBank Accession No. X14945.1, U3 small nuclear RNA gene.

SEQ ID NO: 155 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-B3, distal end. The human homolog is the (+) strand of GenBank Accession No. AL365203.19, integrin, beta 1 (ITGB1).

20 SEQ ID NO: 156 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-B3, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL365203.19, ITGB1.

SEQ ID NO: 157 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-E3, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL365203.19, ITGB1.

25 SEQ ID NO: 158 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-E3, distal end. The human homolog is the (-) strand of GenBank Accession No. AL365203.19, ITGB1.

SEQ ID NO: 159 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-E1, distal end. The human homolog is the  
30 (+) strand of GenBank Accession No. AP001132.4, acrosomal vesicle protein 1 (ACRV1) and CHK1 checkpoint homolog (CHEK1).

SEQ ID NO: 160 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-E5, distal end. The human homolog is the (-) strand of GenBank Accession No. AK025453.1, prospero-related homeobox 1 (PROX1).

35 SEQ ID NO: 161 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E1, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

SEQ ID NO: 162 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E2, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

5 SEQ ID NO: 163 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E3, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

SEQ ID NO: 164 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E4, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

10 SEQ ID NO: 165 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E4, distal end. The human homolog is the (-) strand of GenBank Accession No. AL590543.8, between hypothetical proteins FLJ20627 and FLJ12910.

15 SEQ ID NO: 166 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E5, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

SEQ ID NO: 167 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E8, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

20 SEQ ID NO: 168 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E9, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

25 SEQ ID NO: 169 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E9, distal end. The human homolog is the (-) strand of GenBank Accession No. AL590543.8, between hypothetical proteins FLJ20627 and FLJ12910.

SEQ ID NO: 170 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E10, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

30 SEQ ID NO: 171 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E10, distal end. The human homolog is the (-) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

35 SEQ ID NO: 172 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV19-E2, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

SEQ ID NO: 173 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV19-E2, distal end. The human homolog is the (-) strand of GenBank Accession No. AL590543.8, between hypothetical proteins FLJ20627 and FLJ12910.

SEQ ID NO: 174 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E1, distal end. The human homolog is the (+) strand of GenBank Accession No. AC105001.3, between PIN2-interacting protein 1 (PINX1) and SRY (sex-determining region Y)-box7 (SOX7).

5 SEQ ID NO: 175 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E2, distal end. The human homolog is the (-) strand of GenBank Accession No. AC009520.16, LOC131920.

10 SEQ ID NO: 176 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E3, distal end. The human homolog is the (-) strand of GenBank Accession No. AL596329.5, a region of chromosome 13q14.

SEQ ID NO: 177 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E5, distal end. The human homolog is the (+) strand of GenBank Accession No. AC023844.6, neurotrophic tyrosine kinase, receptor, type 3 (NTRK3).

15 SEQ ID NO: 178 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E7, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC024940.39, between TERA protein (TERA) and hypothetical protein FLJ13224.

20 SEQ ID NO: 179 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E7, distal end. The human homolog is the (+) strand of GenBank Accession No. AC024940.39, flanking TERA protein (TERA) and hypothetical protein FLJ13224.

25 SEQ ID NO: 180 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E8, distal end. The human homolog is the (-) strand of GenBank Accession No. AC084335.6, hypothetical gene LOC284260.

SEQ ID NO: 181 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E11, proximal end. The human homolog is the (+) strand of GenBank Accession No. AC073108.9, POM (POM121 homolog) and ZP3 fusion (POMZP3).

30 SEQ ID NO: 182 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E11, distal end. The human homolog is the (-) strand of GenBank Accession No. AC073108.9, POM (POM121 homolog) and ZP3 fusion (POMZP3).

35 SEQ ID NO: 183 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV19-E4, distal end. The human homolog is the (+) strand of GenBank Accession No. AC087650.12, between DEAD/H box polypeptide 8 (DDX8) and similar to ribosomal protein L29 (cell surface heparin binding protein HIP) (LOC284064).

SEQ ID NO: 184 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV20-E2, distal end. The human homolog is the



(-) strand of GenBank Accession No. AC105285.3, LOC345307 and UDP-N-acetyl-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNT7).

5 SEQ ID NO: 185 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV20-E2, proximal end. The human homolog is the (+) strand of GenBank Accession No. AC105285.3, LOC345307 and UDP-N-acetyl-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNT7).

10 SEQ ID NO: 186 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV20-B1, distal end. The human homolog is the (+) strand of GenBank Accession No. AC105285.3, LOC345307 and UDP-N-acetyl-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNT7).

SEQ ID NO: 187 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV20-E3, distal end. The murine homolog is the (+) strand of GenBank Accession No. NG\_001440.1, *Mus musculus* 5S rRNA pseudogene (Rn5s-ps1).

15 SEQ ID NO: 188 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV20-E5, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL121886.22, between ribosomal protein L27a pseudogene (RPL27AP) and v-myb myeloblastosis viral oncogene homolog-like 2 (MYBL2).

20 SEQ ID NO: 189 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E2, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL121886.22, between RPL27AP and MYBL2.

SEQ ID NO: 190 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E6, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL121886.22, between RPL27AP and MYBL2.

25 SEQ ID NO: 191 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E9, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL121886.22, between RPL27AP and MYBL2.

30 SEQ ID NO: 192 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E9, distal end. The human homolog is the (-) strand of GenBank Accession No. AL121886.22, between RPL27AP and MYBL2.

SEQ ID NO: 193 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV20-E6, distal end. The human homolog is the (+) strand of GenBank Accession No. AP000711.4, Down's syndrome cell adhesion molecule like 1 (DSCAML1).

35 SEQ ID NO: 194 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV20-E7, distal end. The human homolog is the (+) strand of GenBank Accession No. AL391555.19, LOC148529.

SEQ ID NO: 195 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV20-B4, distal end. The human homolog is the

(-) strand of GenBank Accession No. AC112129.4, Huntingtin-associated protein interacting protein (HAPIP).

SEQ ID NO: 196 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. Z69732.1, between LOC158525 and similar to RIKEN cDNA 1210001E11 (LOC347366).

SEQ ID NO: 197 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E3, proximal end. The human homolog is the (-) strand of GenBank Accession No. Z69732.1, between LOC158525 and similar to RIKEN cDNA 1210001E11 (LOC347366).

SEQ ID NO: 198 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E5, proximal end. The human homolog is the (-) strand of GenBank Accession No. Z69732.1, between LOC158525 and similar to RIKEN cDNA 1210001E11 (LOC347366).

SEQ ID NO: 199 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E5, proximal end. The human homolog is the (-) strand of GenBank Accession No. Z69732.1, between LOC158525 and similar to RIKEN cDNA 1210001E11 (LOC347366).

SEQ ID NO: 200 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E8, proximal end. The human homolog is the (-) strand of GenBank Accession No. Z69732.1, between LOC158525 and similar to RIKEN cDNA 1210001E11 (LOC347366).

SEQ ID NO: 201 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E2, distal end. The human homolog is the (-) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ12910.

SEQ ID NO: 202 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E2, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ12910.

SEQ ID NO: 203 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E6, distal end. The human homolog is the (-) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ12910.

SEQ ID NO: 204 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E6, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ12910.

SEQ ID NO: 205 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E7, distal end. The human homolog is the (+) strand of GenBank Accession No. AC005284.1, LOC350411.

SEQ ID NO: 206 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E9, proximal end. The human homolog is

the (+) strand of GenBank Accession No. AP000505.1, between allograft inflammatory factor 1 (AIF1) and HLA-B associated transcript 2 (BAT2).

SEQ ID NO: 207 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV27-E1, distal end. The human homolog is the  
5 (-) strand of GenBank Accession No. AC008755.8, C19orf7.

SEQ ID NO: 208 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV27-E2, distal end. The human homolog is the (+) strand of GenBank Accession No. AC058791.4, between LOC346658 and LOC340349.

SEQ ID NO: 209 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV27-E2, proximal end. The human homolog is the  
10 the (-) strand of GenBank Accession No. AC058791.4, between LOC346658 and LOC340349.

SEQ ID NO: 210 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV27-E3, distal end. The human homolog is the (+) strand of GenBank Accession No. AC079030.13, a region of chromosome 12q21.

SEQ ID NO: 211 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV27-E3, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC139138.2, between LOC339248 and hypothetical protein  
15 FLJ22659.

SEQ ID NO: 212 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV27-E4, distal end. The human homolog is the  
20 (-) strand of GenBank Accession No. AL513550.9, between SR rich protein DKFZp564B0769 and hypothetical protein MGC14793.

SEQ ID NO: 213 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-B1, distal end. The human homolog is the  
25 (-) strand of GenBank Accession No. AP001160.4, hypothetical protein FLJ10439.

SEQ ID NO: 214 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-B1, proximal end. The human homolog is the (+) strand of GenBank Accession No. AP001160.4, hypothetical protein FLJ10439.

SEQ ID NO: 215 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-B3, distal end. The human homolog is the  
30 (+) strand of GenBank Accession No. AC090826.15, between cytochrome P450, family 11, subfamily A, polypeptide 1 (CYP11A1) and sema domain, immunoglobulin domain (Ig) and GPI membrane anchor, (semaphoring) 7A.

SEQ ID NO: 216 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-B3, proximal end. The human homolog is  
35 the (-) strand of GenBank Accession No. AC090826.15, between cytochrome P450, family 11, subfamily A, polypeptide 1 (CYP11A1) and sema domain, immunoglobulin domain (Ig) and GPI membrane anchor, (semaphoring) 7A.

SEQ ID NO: 217 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E11, proximal end. The human homolog is the (+) strand of GenBank Accession No. AC090826.15, between cytochrome P450, family 11, subfamily A, polypeptide 1 (CYP11A1) and sema domain, immunoglobulin domain (Ig) and GPI membrane anchor, (semaphoring) 7A.

SEQ ID NO: 218 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E11, distal end. The human homolog is the (-) strand of GenBank Accession No. AC090826.15, between cytochrome P450, family 11, subfamily A, polypeptide 1 (CYP11A1) and sema domain, immunoglobulin domain (Ig) and GPI membrane anchor, (semaphoring) 7A.

SEQ ID NO: 219 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC011500.7, ribosomal protein S16 (RPS16).

SEQ ID NO: 220 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E1, distal end. The human homolog is the (+) strand of GenBank Accession No. AC011500.7, ribosomal protein S16 (RPS16).

SEQ ID NO: 221 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E4, distal end. The human homolog is the (-) strand of GenBank Accession No. AC091172.11, between hypothetical protein DKFZp434H0115 and ATP citrate lyase (ACLY).

SEQ ID NO: 222 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E4, proximal end. The human homolog is the (+) strand of GenBank Accession No. AC091172.11, between hypothetical protein DKFZp434H0115 and ACLY.

SEQ ID NO: 223 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E7, distal end. The human homolog is the (+) strand of GenBank Accession No. AL035594.7, protein tyrosine phosphatase, receptor type, K (PTPRK).

SEQ ID NO: 224 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E7, proximal end. The human homolog is the (+) strand of GenBank Accession No. AC124857.2, calnexin (CANX) and (-) strand of GenBank Accession No. AL035594.7, protein tyrosine phosphatase, receptor type, K (PTPRK).

SEQ ID NO: 225 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E8, distal end. The human homolog is the (+) strand of GenBank Accession No. AC009144.5, cyclin M2 (CNNM2).

SEQ ID NO: 226 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E8, proximal end. The human homolog is the (+) strand of GenBank Accession No. AC011510.7, AXL receptor tyrosine kinase (AXL).

SEQ ID NO: 227 is a nucleic acid sequence showing GenBank Accession No. BC008947, *Homo sapiens* chromosome 10 open reading frame 3, mRNA (cDNA clone MGC:3422 IMAGE:3028566). This sequence is associated with viral infection, such as Ebola infection.

SEQ ID NO: 228 is an amino acid sequence encoded by SEQ ID NO: 227.

5 SEQ ID NO: 229 is a nucleic acid sequence showing GenBank Accession No. NM\_018131, *Homo sapiens* chromosome 10 open reading frame 3 (C10orf3). This sequence is associated with viral infection, such as Ebola infection.

SEQ ID NO: 230 is an amino acid sequence encoded by SEQ ID NO: 229.

10 SEQ ID NO: 231 is a nucleic acid sequence showing GenBank Accession No. NM\_013451, *Homo sapiens fer-1-like 3, myoferlin (C. elegans) (FER1L3)*, transcript variant 1, mRNA. This sequence is associated with viral infection, such as Ebola infection.

SEQ ID NO: 232 is an amino acid sequence encoded by SEQ ID NO: 231.

SEQ ID NOS: 233 and 234 are exemplary complementary primers.

15 SEQ ID NOS: 235-237 are primer sequences used to sequence the shuttle clones as described in Example 2.

SEQ ID NOS: 238-241 are Rab9 siRNA sequences.

SEQ ID NOS: 242-245 are AXL receptor tyrosine kinase siRNA sequences.

SEQ ID NOS: 246-295 are beta-chimerin receptor tyrosine kinase RNAi sequences.

20 SEQ ID NOS: 296-345 are retinoblastoma binding protein 1 RNAi sequences.

SEQ ID NOS: 346-395 are *Homo sapiens* chromosome 10 open reading frame 3 RNAi sequences.

SEQ ID NOS: 396-445 are *Homo sapiens fer-1-like 3, myoferlin (C. elegans)*, transcript variant 1 RNAi sequences.

25 SEQ ID NOS: 446-495 are *Homo sapiens* chromosome 10 open reading frame 3 (C10orf3) RNAi sequences.

SEQ ID NOS: 496-545 are malic enzyme RNAi sequences.

SEQ ID NOS: 546-595 are cadherin related 23 RNAi sequences.

SEQ ID NOS: 596-645 are sideroflexin 5 RNAi sequences.

SEQ ID NOS: 646-695 are polybromo 1 (PB1) RNAi sequences.

30 SEQ ID NOS: 696-720 are elongation factor for selenoprotein translation RNAi sequences.

SEQ ID NOS: 721-745 are integrin, beta 1 RNAi sequences.

SEQ ID NOS: 746-795 are huntingtin interacting protein 1 RNAi sequences.

SEQ ID NOS: 796-845 are cyclin M2 RNAi sequences.

35

## DETAILED DESCRIPTION OF SEVERAL EMBODIMENTS

### Abbreviations and Terms

The following explanations of terms and methods are provided to better describe the present disclosure and to guide those of ordinary skill in the art in the practice of the present disclosure. The singular forms "a," "an," and "the" refer to one or more than one, unless the context clearly dictates

otherwise. For example, the term "comprising a nucleic acid" includes single or plural nucleic acids and is considered equivalent to the phrase "comprising at least one nucleic acid." The term "or" refers to a single element of stated alternative elements or a combination of two or more elements, unless the context clearly indicates otherwise. For example, the phrase "a first nucleic acid or a second nucleic acid" refers to the first nucleic acid, the second nucleic acid, or a combination of both the first and second nucleic acids. As used herein, "comprises" means "includes." Thus, "comprising a promoter and an open reading frame," means "including a promoter and an open reading frame," without excluding additional elements.

Unless explained otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this disclosure belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present disclosure, suitable methods and materials are described below. The materials, methods, and examples are illustrative only and not intended to be limiting.

A = adenine  
C = cytosine  
DNA = deoxyribonucleic acid  
ds = double-stranded (for example, dsDNA)  
G = guanine  
mg = milligram  
ng = nanogram  
PCR = polymerase chain reaction  
Pu = purine  
Py = pyrimidine  
RNA = ribonucleic acid  
mRNA = messenger RNA  
MOI = multiplicity of infection  
siRNA = short interfering or interrupting RNA  
ss = single-stranded (for example, ssDNA)  
T = thymine  
T<sub>m</sub> = melting temperature  
U = uracil  
μg = microgram  
μl = microliter

**Amplification of a nucleic acid.** To increase the number of copies of a nucleic acid. Several methods can be used to amplify a nucleic acid, such as polymerase chain reaction (PCR). Other examples of amplification include, but are not limited to, strand displacement amplification (U.S. Patent No: 5,744,311); transcription-free isothermal amplification (U.S. Patent No: 6,033,881);

repair chain reaction amplification (WO 90/01069); ligase chain reaction amplification (European Patent Appl. 320 308); gap filling ligase chain reaction amplification (U.S. Patent No: 5,427,930); and NASBA™ RNA transcription-free amplification (U.S. Patent No: 6,025,134).

5 The amplification products ("amplicons") can be further processed, manipulated, or characterized by electrophoresis, restriction endonuclease digestion, hybridization, nucleic acid sequencing, ligation, or other molecular biology techniques. Standard protocols can be modified. For example, PCR can be modified by using reverse transcriptase PCR (RT-PCR) to amplify RNA molecules.

10 Antisense, Sense, and Antigene. Antisense molecules are molecules that are specifically hybridizable or specifically complementary to either RNA or the plus strand of DNA. Sense molecules are molecules that are specifically hybridizable or specifically complementary to the minus strand of DNA. Antigene molecules are either antisense or sense molecules directed to a particular dsDNA target. These molecules can be used to interfere with gene expression.

15 Double-stranded DNA (dsDNA) has two strands, a 5' to 3' strand, referred to as the plus (+) strand, and a 3' to 5' strand (the reverse complement), referred to as the minus (-) strand. Because RNA polymerase adds nucleic acids in a 5' to 3' direction, the minus strand of the DNA serves as the template for the RNA during transcription. Thus, the RNA formed will have a sequence complementary to the minus strand and virtually identical to the plus strand, except that U is substituted for T in RNA molecules.

20 Array. An arrangement of biological samples or molecules, such as an arrangement of tissues, cells, or biological macromolecules (including, but not limited to, peptides or nucleic acids) in addressable locations on or in a substrate. The arrangement of molecules within the array can be regular, such as being arranged in uniform rows and columns, or irregular. The number of addressable locations within the array can vary, for example from a few (such as two or three) to  
25 more than 50, 100, 200, 500, 1000, 10,000, or more. In certain examples, the array includes one or more molecules or samples occurring on the array a plurality of times (twice or more) to provide an added feature to the array, such as redundant activity or to provide internal controls. A "microarray" is an array that is miniaturized and evaluated or analyzed using microscopy.

30 Within an array, each arrayed sample or molecule is addressable, such that its location can be reliably and consistently determined within the at least two dimensions of the array. The location or address of each sample or molecule can be assigned when it is applied to the array, and a key or guide can be provided in order to correlate each location with the appropriate target sample or molecule position. Ordered arrays can be arranged in a symmetrical grid pattern or other patterns, for example, in radially distributed lines, spiral lines, or ordered clusters. Addressable arrays can be  
35 computer readable; a computer can be programmed to correlate a particular address on the array with information about the sample at that position, such as hybridization or binding data, including signal intensity. In some exemplary computer readable formats, the individual samples or molecules in the array are arranged regularly (for example, in a Cartesian grid pattern), which can be correlated to address information by a computer.

The sample or molecule addresses on an array can assume many different shapes. For example, substantially square regions can be used as addresses within arrays, but addresses can be differently shaped, for example, substantially rectangular, triangular, oval, irregular, or another shape. The term "spot" refers generally to a localized placement of molecules, tissue or cells, and is not limited to a round or substantially round region or address.

Examples of macroarrays include the Histo™-array and INSTA-blot™ lines of products available from Imgenix, Inc. (San Diego, CA) and the Max Array™ line of products available from Zymed Laboratories, Inc. (South San Francisco, CA), while exemplary microarrays include the various GeneChip® technologies and products available from Affymetrix, Inc. (Santa Clara, CA) and the Hilight™, Label Star™, and Array-Ready Oligo Set lines of products available from Qiagen, Inc. (Valencia, CA).

**β-chimerin.** The term β-chimerin includes any β-chimerin gene, cDNA, RNA, or protein from any organism and is a β-chimerin that can function as a type of rho-GTPase. In some examples, β-chimerin is involved in viral infection.

Rho-GTPases are a family of small GTPases implicated as components of cellular signal transduction cascades. Signals that pass through rho-GTPase cascades can be initiated by the activation of cell surface proteins, such as growth factors. Functions of signaling cascades mediated by rho-GTPases, include, but are not limited to, alterations in cellular morphology which are linked to processes such as immune cell function, oncogenesis, metastasis and certain diseases (Peck, *FEBS Lett.* 528:27, 2002).

Examples of native β-chimerin nucleic acid sequences include, but are not limited to those shown in SEQ ID NOS: 21-22 (such as a target sequence associated with SEQ ID NOS: 21-22), as well as the protein sequence encoded thereby. This cell line remains CD4<sup>+</sup> after exposure to HIV 1 and HIV 2 and is resistant to HIV infection. β-chimerin also includes variants, fusions, and fragments of the disclosed nucleic acid and amino acid sequences that retain β-chimerin biological activity.

Examples of β-chimerin amino acid sequences include, but are not limited to: Genbank Accession Nos: NM\_004067 (mRNA) and NP\_004058.1 (protein). In one example, a β-chimerin sequence includes a full-length wild-type (or native) sequence, as well as β-chimerin allelic variants, variants, fragments, homologs or fusion sequences that retain the ability to function as a type of rho-GTPase. In certain examples, β-chimerin has at least 80% sequence identity, for example at least 85%, 90%, 95%, or 98% sequence identity to a native β-chimerin.

**cDNA (complementary DNA).** A piece of DNA lacking internal, non-coding segments (introns) and transcriptional regulatory sequences. A cDNA also can contain untranslated regions (UTRs) that are responsible for translational control in the corresponding RNA molecule. cDNA can be produced using various methods, such as synthesis in the laboratory by reverse transcription from messenger RNA extracted from cells.

**Complementary.** Complementary binding occurs when the base of one nucleic acid molecule forms a hydrogen bond the base of another nucleic acid molecule. Normally, the base



adenine (A) is complementary to thymidine (T) and uracil (U), while cytosine (C) is complementary to guanine (G). For example, the sequence 5'-ATCG-3' of one ssDNA molecule can bond to 3'-TAGC-5' of another ssDNA to form a dsDNA.

Nucleic acid molecules can be complementary to each other even without complete hydrogen-bonding of all bases of each molecule. By way of example only (and without limitation), the ssDNA: 5'-GCTTGCCAAACCTACA-3' (SEQ ID NO: 233) is considered complementary to the ssDNA 3'-CGAACGGTCTGGATGT-5' (SEQ ID NO: 234) even though there is a mismatched base pair (A-C rather than A-T or G-C) at the ninth position.

Conservative substitution: A substitution of an amino acid residue for another amino acid residue having similar biochemical properties. Typically, conservative substitutions have little to no impact on the biological activity of a resulting polypeptide. In a particular example, a conservative substitution is an amino acid substitution in a peptide that does not substantially affect the biological function of the peptide. A peptide can include one or more amino acid substitutions, for example 2-10 conservative substitutions, 2-5 conservative substitutions, 4-9 conservative substitutions, such as 2, 5 or 10 conservative substitutions.

For example, a conservative substitution in a  $\beta$ -chimerin peptide (such as a peptide encoded by a target sequence associated with SEQ ID NO: 21 or 22) does not substantially affect the ability of  $\beta$ -chimerin to confer resistance to HIV infection. In another example, a conservative substitution in a Rab9 peptide (such as a peptide encoded by a target sequence associated with SEQ ID NOS: 118 or 119) is one that does not substantially affect the ability of Rab9 to confer resistance to infection by a pathogen that can hijack a lipid raft, such as HIV or Ebola.

A polypeptide can be produced to contain one or more conservative substitutions by manipulating the nucleotide sequence that encodes that polypeptide using, for example, standard procedures such as site-directed mutagenesis or PCR. Alternatively, a polypeptide can be produced to contain one or more conservative substitutions by using standard peptide synthesis methods. An alanine scan can be used to identify which amino acid residues in a protein can tolerate an amino acid substitution. In one example, the biological activity of the protein is not decreased by more than 25%, for example not more than 20%, for example not more than 10%, when an alanine, or other conservative amino acid (such as those listed below), is substituted for one or more native amino acids.

Examples of amino acids which can be substituted for an original amino acid in a protein and which are regarded as conservative substitutions include, but are not limited to: Ser for Ala; Lys for Arg; Gln or His for Asn; Glu for Asp; Ser for Cys; Asn for Gln; Asp for Glu; Pro for Gly; Asn or Gln for His; Leu or Val for Ile; Ile or Val for Leu; Arg or Gln for Lys; Leu or Ile for Met; Met, Leu or Tyr for Phe; Thr for Ser; Ser for Thr; Tyr for Trp; Trp or Phe for Tyr; and Ile or Leu for Val.

Further information about conservative substitutions can be found in, among other locations in, Ben-Bassat *et al.*, (*J. Bacteriol.* 169:751-7, 1987), O'Regan *et al.*, (*Gene* 77:237-51, 1989), Sahin-

Toth *et al.*, (*Protein Sci.* 3:240-7, 1994), Hochuli *et al.*, (*Bio/Technology* 6:1321-5, 1988) and in standard textbooks of genetics and molecular biology.

**Ebola virus.** A highly contagious hemorrhagic virus named after a river in the Democratic Republic of the Congo (formerly Zaire) in Africa, where it was first recognized. Ebola is one of two members of a family of RNA viruses called the Filoviridae. There are four identified subtypes of Ebola virus. Three of the four have caused disease in humans: Ebola-Zaire, Ebola-Sudan, and Ebola-Ivory Coast. The fourth, Ebola-Reston, has caused disease in nonhuman primates, but not in humans.

Ebola hemorrhagic fever (Ebola HF) is a severe, often fatal disease in humans and nonhuman primates (for example, monkeys, gorillas, and chimpanzees) that is caused by Ebola virus infection. Diagnosing Ebola HF in a recently infected individual can be difficult because early symptoms, such as red eyes and a skin rash, are nonspecific to the virus and are seen in other subjects with diseases that occur much more frequently. Antigen-capture enzyme-linked immunosorbent assay (ELISA) testing, IgM ELISA, PCR, and virus isolation can be used to diagnose a case of Ebola HF within a few days after the onset of symptoms. Subjects tested later in the course of the disease, or after recovery, can be tested for IgM and IgG antibodies. The disease also can be diagnosed retrospectively in deceased patients by using immunohistochemistry testing, virus isolation, or PCR.

**Encodes:** Unless evident from its context, includes DNA sequences that encode a polypeptide, as the term is typically used, as well as DNA sequences that are transcribed into inhibitory antisense molecules.

**Expression:** With respect to a gene sequence, refers to transcription of the gene and, as appropriate, translation of the resulting mRNA transcript to a protein. Thus, expression of a protein coding sequence results from transcription and translation of the coding sequence.

**Functional deletion:** A mutation, partial or complete deletion, insertion, or other variation made to a gene sequence that inhibits production of the gene product or renders the gene product non-functional. For example, a functional deletion of a Rab9 gene in a cell results in a cells having non-functional Rab9 protein, which results in the cell having an increase resistance to infection by a pathogen that uses a lipid raft.

**Gene.** A nucleic acid sequence that encodes a polypeptide under the control of a regulatory sequence, such as a promoter or operator. A gene includes an open reading frame encoding a polypeptide of the present disclosure, as well as exon and (optionally) intron sequences. An intron is a DNA sequence present in a given gene that is not translated into protein and is generally found between exons. The coding sequence of the gene is the portion transcribed and translated into a polypeptide (*in vivo*, *in vitro* or *in situ*) when placed under the control of an appropriate regulatory sequence. The boundaries of the coding sequence can be determined by a start codon at the 5' (amino) terminus and a stop codon at the 3' (carboxyl) terminus. If the coding sequence is intended to be expressed in a eukaryotic cell, a polyadenylation signal and transcription termination sequence can be included 3' to the coding sequence.

Transcriptional and translational control sequences include, but are not limited to, DNA regulatory sequences such as promoters, enhancers, and terminators that provide for the expression of

the coding sequence, such as expression in a host cell. A polyadenylation signal is an exemplary eukaryotic control sequence. A promoter is a regulatory region capable of binding RNA polymerase and initiating transcription of a downstream (3' direction) coding sequence. Additionally, a gene can include a signal sequence at the beginning of the coding sequence of a protein to be secreted or expressed on the surface of a cell. This sequence can encode a signal peptide, N-terminal to the mature polypeptide, which directs the host cell to translocate the polypeptide.

**Host Cell.** Any cell that can be infected with a virus or other pathogen, such as a bacterium. A host cell can be prokaryotic or eukaryotic, such as a cell from an insect, crustacean, mammal, bird, reptile, yeast, or a bacteria such as *E. coli*. Exemplary host cells include, but are not limited to, mammalian B-lymphocyte cells. Examples of viruses include, but are not limited to HIV, influenza A, and Ebola.

The host cell can be part of an organism, or part of a cell culture, such as a culture of mammalian cells or a bacterial culture. A host nucleic acid is a nucleic acid present in a host cell that expresses a host protein. Decreasing or inhibiting the interaction between a host polypeptide or host nucleic acid and a virus or viral protein can occur *in vitro*, *in vivo*, and *in situ* environments.

**Human Immunodeficiency Virus (HIV).** A retrovirus that causes immunosuppression in humans and leads to a disease complex known as acquired immunodeficiency syndrome (AIDS). This immunosuppression results from a progressive depletion and functional impairment of T lymphocytes expressing the CD4 cell surface glycoprotein. The loss of CD4 helper/inducer T cell function may underlie the loss of cellular and humoral immunity leading to the opportunistic infections and malignancies seen in AIDS.

Depletion of CD4 T cells results from the ability of HIV to selectively infect, replicate in, and ultimately destroy these T cells (for example see Klatzmann *et al.*, *Science* 225:59, 1984). CD4 itself is an important component, and in some examples an essential component, of the cellular receptor for HIV.

HIV subtypes can be identified by particular number, such as HIV-1 and HIV-2. In the HIV life cycle, the virus enters a host cell in at least three stages: receptor docking, viral-cell membrane fusion, and particle uptake (D'Souza *et al.*, *JAMA* 284:215, 2000). Receptor docking begins with a gp120 component of a virion spike binding to the CD4 receptor on the host cell. Conformational changes in gp120 induced by gp120-CD4 interaction promote an interaction between gp120 and either CCR5 or CXCR4 cellular co-receptors. The gp41 protein then mediates fusion of the viral and target-cell membranes. More detailed information about HIV can be found in Coffin *et al.*, *Retroviruses* (Cold Spring Harbor Laboratory Press, 1997).

**Hybridization.** Hybridization of a nucleic acid occurs when two complementary nucleic acid molecules undergo an amount of hydrogen bonding to each other. The stringency of hybridization can vary according to the environmental conditions surrounding the nucleic acids, the nature of the hybridization method, and the composition and length of the nucleic acids used. For example, temperature and ionic strength (such as Na<sup>+</sup> concentration) can affect the stringency of hybridization. Calculations regarding hybridization conditions required for attaining particular

degrees of stringency are discussed in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 2001); and Tijssen, *Laboratory Techniques in Biochemistry and Molecular Biology—Hybridization with Nucleic Acid Probes Part I*, Chapter 2 (Elsevier, New York, 1993).

5           The  $T_m$  is the temperature at which 50% of a given strand of nucleic acid is hybridized to its complementary strand. The  $T_m$  of a particular nucleic acid can be determined by various methods, such as observing the transition state between a single-stranded and double-stranded state during a temperature change, such as heating a dsDNA from about 30°C to about 100°C, and detecting when the dsDNA denatures to ssDNA. This can be accomplished by determining a melting profile for the  
10       nucleic acid. For longer nucleic acid fragments, such as PCR products, the nearest-neighbor method can be used to determine  $T_m$  (Breslauer *et al.*, *Proc. Natl. Acad. Sci. USA* 83:3746-50, 1986). Additionally, MeltCalc software can be used to determine  $T_m$  (Schütz and von Ahsen, *Biotechniques* 30:8018-24, 1999).

For purposes of this disclosure, "stringent conditions" encompass conditions under which  
15       hybridization only will occur if there is less than 25% mismatch between the hybridization molecule and the target sequence. "Moderate stringency" conditions are those under which molecules with more than 25% sequence mismatch will not hybridize; conditions of "medium stringency" are those under which molecules with more than 15% mismatch will not hybridize, and conditions of "high stringency" are those under which sequences with more than 10% mismatch will not hybridize.  
20       Conditions of "very high stringency" are those under which sequences with more than 5% mismatch will not hybridize.

Moderately stringent hybridization conditions are when the hybridization is performed at about 42°C in a hybridization solution containing 25 mM  $KPO_4$  (pH 7.4), 5X SSC, 5X Denhart's solution, 50 µg/mL denatured, sonicated salmon sperm DNA, 50% formamide, 10% Dextran sulfate,  
25       and 1-15 ng/mL probe (about  $5 \times 10^7$  cpm/µg), while the washes are performed at about 50°C with a wash solution containing 2X SSC and 0.1% sodium dodecyl sulfate.

Highly stringent hybridization conditions are when the hybridization is performed at about 42°C in a hybridization solution containing 25 mM  $KPO_4$  (pH 7.4), 5X SSC, 5X Denhart's solution, 50 µg/mL denatured, sonicated salmon sperm DNA, 50% formamide, 10% Dextran sulfate, and 1-15  
30       ng/mL probe (about  $5 \times 10^7$  cpm/µg), while the washes are performed at about 65°C with a wash solution containing 0.2X SSC and 0.1% sodium dodecyl sulfate.

**Infection.** The entry, replication, insertion, lysis or other event or process involved with the pathogenesis of a virus or other infectious agent into a host cell. Thus, decreasing infection includes decreasing entry, replication, insertion, lysis, or other pathogenesis of a virus or other pathogen into a  
35       cell or subject, or combinations thereof. Infection includes the introduction of an infectious agent, such as a non-recombinant virus, recombinant virus, plasmid, bacteria, prion, eukaryotic microbe, or other agent capable of infecting a host, such as the cell of a subject.

In another example, infection is the introduction of a recombinant vector into a host cell via transduction, transformation, transfection, or other method. Vectors include, but are not limited to,

viral, plasmid, cosmid, and artificial chromosome vectors. For example, a recombinant vector can include an antisense molecule, RNAi molecule, or siRNA that recognizes any target sequences associated with SEQ ID NOS: 1-227, 229, and 231, or variants, fusions, or fragments thereof, as well as SEQ ID NOS: 1-227, 229, and 231 themselves.

5           **Influenza virus.** A virus that causes respiratory disease or influenza ("the flu") and can lead to a secondary infection in the host, such as a bacterial infection of the lungs. Three types of influenza are currently known: influenza A, influenza B, and influenza C. Influenza A is the most common form of the virus and is capable of infection humans and non-human animals, such as pigs, horses, chickens, ducks and other birds.

10           The viral genome includes eight RNA molecules. HA, which encodes hemagglutinin (three hemagglutinin subtypes: H1, H2, and H3); M, which encodes two matrix proteins based on two different open reading frames within the nucleic acid sequence; NA encodes for neuraminidase; NP encodes the nucleoprotein; NS encodes two non-structural proteins based on different open reading frames within the nucleic acid sequence; and three genes that encode RNA polymerases (PA, PB1, PB2). The influenza virus can be categorized into subtypes on the bases of the surface glycoproteins.

15           The replication cycle of the influenza virus begins with binding of the viral hemagglutinin molecules to the surface carbohydrate of epithelial cell of a host cell, which draws the virus into the cell by receptor-mediated endocytosis. The viral membrane fuses with the endocytotic vesicle membrane, allowing the RNA molecules of the viral genome to enter the interior of the cell where these molecules later enter the cell nucleus and are replicated into viral-complementary RNA and new viral RNA and transcribed into viral mRNA, which are transported into the cytosol where they are translated into the proteins of new viral particles. After viral particles are assembled into new viruses, the neuraminidase glycoproteins proteins aid in the budding of the viruses from the cellular membrane of the host cell, thus releasing new viruses capable of infecting other host cells.

20           **Isolated:** An "isolated" biological component (such as a nucleic acid or protein) has been substantially separated, produced apart from, or purified away from other biological components in the cell of the organism in which the component naturally occurs, such as other chromosomal and extrachromosomal DNA and RNA, and proteins. Nucleic acids and proteins which have been "isolated" include nucleic acids and proteins purified by standard purification methods. The term  
25           also embraces nucleic acids and proteins prepared by recombinant expression in a host cell as well as chemically synthesized nucleic acids, proteins and peptides.

30           **Nucleic acid.** A deoxyribonucleotide or ribonucleotide polymer in either single (ss) or double stranded (ds) form, and can include analogues of natural nucleotides that hybridize to nucleic acids in a manner similar to naturally occurring nucleotides. In some examples, a nucleic acid is a  
35           nucleotide analog.

          Unless otherwise specified, any reference to a nucleic acid molecule includes the reverse complement of nucleic acid. Except where single-strandedness is required by the text herein (for example, a ssRNA molecule), any nucleic acid written to depict only a single strand encompasses both strands of a corresponding double-stranded nucleic acid. For example, depiction of a plus-strand

of a dsDNA also encompasses the complementary minus-strand of that dsDNA. Additionally, reference to the nucleic acid molecule that encodes a specific protein, or a fragment thereof, encompasses both the sense strand and its reverse complement.

In particular examples, a nucleic acid includes a nucleotide sequence shown in any of SEQ ID NOS: 1-227, 229, and 231, or a variant, fragment, or fusion thereof. In other examples, a nucleic acid has a nucleotide sequence including a target sequence associated with SEQ ID NOS: 1-227, 229, and 231, or a variant, fragment, or fusion thereof, such as the corresponding cDNA or mRNA of SEQ ID NOS: 1-227, 229, and 231.

The fragment can be any portion of the nucleic acid corresponding to at least 5 contiguous bases from any target nucleic acid sequence associated with SEQ ID NOS: 1-227, 229, and 231, for example at least 20 contiguous bases, at least 50 contiguous bases, at least 100 contiguous bases, at least 250 contiguous bases, or even at least 500 or more contiguous bases. A fragment can be chosen from a particular portion of any of the target sequences associated with SEQ ID NOS: 1-227, 229, and 231, such as a particular half, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth, or smaller portion of any of the target sequences associated with SEQ ID NOS: 1-227, 229, and 231. Fragments of the nucleic acids described herein can be used as probes and primers.

**Oligonucleotide.** A linear polynucleotide (such as DNA or RNA) sequence of at least 9 nucleotides, for example at least 15, 18, 24, 25, 30, 50, 100, 200 or even 500 nucleotides long. In particular examples, an oligonucleotide is about 6-50 bases, for example about 10-25 bases, such as 12-20 bases.

An oligonucleotide analog refers to moieties that function similarly to oligonucleotides, but have non-naturally occurring portions. For example, oligonucleotide analogs can contain non-naturally occurring portions, such as altered sugar moieties or inter-sugar linkages, such as a phosphorothioate oligodeoxynucleotide. Functional analogs of naturally occurring polynucleotides can bind to RNA or DNA, and include peptide nucleic acid (PNA) molecules.

**Open reading frame (ORF).** A series of nucleotide triplets (codons) coding for amino acids without any internal termination codons. These sequences are usually translatable into a peptide.

**Operably linked.** A first nucleic acid sequence is operably linked with a second nucleic acid sequence when the first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Generally, operably linked DNA sequences are contiguous and, where necessary to join two protein coding regions, in the same reading frame.

**Pathogen:** A disease-producing agent. Examples include, but are not limited to viruses, bacteria, and fungi.

**Pharmaceutical agent or drug:** A chemical compound or composition capable of inducing a desired therapeutic or prophylactic effect when administered to a subject, alone or in combination with another therapeutic agent(s) or pharmaceutically acceptable carriers. In a particular example, a

pharmaceutical agent decreases or even inhibits infection of a cell, such as the cell of a subject, by a pathogen, such as a virus.

Polymorphism. A polymorphism exists when two or more versions of a nucleic acid sequence exist within a population of subjects. For example, a polymorphic nucleic acid can be one where the most common allele has a frequency of 99% or less. Different alleles can be identified according to differences in nucleic acid sequences, and genetic variations occurring in more than 1% of a population (which is the commonly accepted frequency for defining polymorphism) are useful polymorphisms for certain applications.

The allelic frequency (the proportion of all allele nucleic acids within a population that are of a specified type) can be determined by directly counting or estimating the number and type of alleles within a population. Polymorphisms and methods of determining allelic frequencies are discussed in Hartl, D.L. and Clark, A.G., *Principles of Population Genetics*, Third Edition (Sinauer Associates, Inc., Sunderland Massachusetts, 1997), particularly in chapters 1 and 2.

Preventing or treating a disease: "Preventing" a disease refers to inhibiting the full development of a disease, for example preventing development of a viral infection. "Treatment" refers to a therapeutic intervention that ameliorates a sign or symptom of a disease or pathological condition related to a viral infection, such as inhibiting or decreasing viral infection.

Probes and primers. A probe includes an isolated nucleic acid attached to a detectable label or other reporter molecule. Typical labels include, but are not limited to radioactive isotopes, enzyme substrates, co-factors, ligands, chemiluminescent or fluorescent agents, haptens, and enzymes. Methods for labeling and guidance in the choice of labels appropriate for various purposes are discussed for example in Sambrook *et al.* (*Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor, New York, 1989) and Ausubel *et al.* (*In Current Protocols in Molecular Biology*, John Wiley & Sons, New York, 1998).

Primers are short nucleic acid molecules, such as DNA oligonucleotides ten nucleotides or more in length. Longer DNA oligonucleotides can be about 15, 20, 25, 30 or 50 nucleotides or more in length. Primers can be annealed to a complementary target DNA strand by nucleic acid hybridization to form a hybrid between the primer and the target DNA strand, and then the primer extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification of a nucleic acid sequence, for example by the polymerase chain reaction (PCR) or other nucleic-acid amplification methods.

Nucleic acid probes and primers can be prepared based on the nucleic acid molecules of the target sequences associated with SEQ ID NOS: 1-227, 229, and 231, as indicators of resistance to infection. Probes and primers can be based on fragments or portions of these nucleic acid molecules, or on the reverse complement of these sequences, as well as probes and primers to 5' or 3' regions of the nucleic acids.

The specificity of a probe or primer increases with its length. Thus, for example, a primer that includes 30 consecutive nucleotides of a  $\beta$ -chimerin or Rab9 gene will anneal to a target sequence, such as another homolog of a  $\beta$ -chimerin or Rab9 gene, respectively, with a higher specificity than a

corresponding primer of only 15 nucleotides. Thus, to obtain greater specificity, probes and primers can be selected that include at least 20, 25, 30, 35, 40, 45, 50 or more consecutive nucleotides of a nucleic acid disclosed herein.

**Protein coding sequence or a sequence that encodes a peptide:** A nucleic acid sequence that is transcribed (in the case of DNA) and is translated (in the case of mRNA) into a peptide *in vitro* or *in vivo* when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a start codon at the 5' (amino) terminus and a translation stop codon at the 3' (carboxy) terminus. A coding sequence can include, but is not limited to, cDNA from procaryotic or eukaryotic mRNA, genomic DNA sequences from procaryotic or eukaryotic DNA, and even synthetic DNA sequences. A transcription termination sequence is usually located 3' to the coding sequence.

**Purified.** The term purified does not require absolute purity; rather, it is a relative term. Thus, for example, a purified peptide preparation is one in which the peptide or protein is more enriched than the peptide or protein is in its environment within a cell, such that the peptide is substantially separated from cellular components (nucleic acids, lipids, carbohydrates, and other polypeptides) that may accompany it. In another example, a purified peptide preparation is one in which the peptide is substantially-free from contaminants, such as those that might be present following chemical synthesis of the peptide.

In one example, an peptide is purified when at least 60% by weight of a sample is composed of the peptide, for example when 75%, 95%, or 99% or more of a sample is composed of the peptide, such as a  $\beta$ -chimerin or Rab9 peptide. Examples of methods that can be used to purify proteins, include, but are not limited to the methods disclosed in Sambrook et al. (Molecular Cloning: A Laboratory Manual, Cold Spring Harbor, New York, 1989, Ch. 17). Protein purity can be determined by, for example, polyacrylamide gel electrophoresis of a protein sample, followed by visualization of a single polypeptide band upon staining the polyacrylamide gel; high-pressure liquid chromatography; sequencing; or other conventional methods.

**Rab9:** The term Rab9 includes any Rab9 gene, cDNA, RNA, or protein from any organism and that is a Rab9 that can transport late endosomes to trans-golgi and function as a ras-like GTPase. In some examples, Rab9 is involved in lipid raft formation.

Examples of native Rab9 nucleic acid sequences include, but are not limited to, target sequences associated with SEQ ID NOS: 118 and 119. Examples of Rab9 amino acid sequences include, but are not limited to: Genbank Accession Nos: BC017265.2 and NM\_004251.3 (cDNA) as well as P51151 and AAH17265 (proteins). In one example, a Rab9 sequence includes a full-length wild-type (or native) sequence, as well as Rab9 allelic variants, variants, fragments, homologs or fusion sequences that retain the ability to transport late endosomes to trans-golgi. In certain examples, Rab9 has at least 80% sequence identity, for example at least 85%, 90%, 95%, or 98% sequence identity to a native Rab9.

In other examples, Rab9 has a sequence that hybridizes to a sequence set forth in GenBank Accession No. BC017265.2 or NM\_004251.3, and retains Rab9 activity.



Recombinant. A recombinant nucleic acid or protein is one that has a sequence that is not naturally occurring or has a sequence that is made by an artificial combination of two otherwise separated segments of sequence. This artificial combination can be accomplished, for example, by chemical synthesis or by the artificial manipulation of isolated segments of nucleic acids or proteins, for example, by genetic engineering techniques.

RNA interference (RNAi): A post-transcriptional gene silencing mechanism mediated by double-stranded RNA (dsRNA). Introduction of dsRNA into cells, such as RNAi compounds or siRNA compounds, induces targeted degradation of RNA molecules with homologous sequences. RNAi compounds are typically longer than an siRNA molecule. For example, an RNAi molecule can be at least about 25 nucleic acids, at least about 27 nucleic acids, or even at least about 400 nucleotides in length.

RNAi compounds can be used to modulate transcription, for example, by silencing genes, such as Rab9,  $\beta$ -chimerin, or combinations thereof. In certain examples, an RNAi molecule is directed against a certain target gene, such as Rab9,  $\beta$ -chimerin, or combinations thereof, and is used to decrease viral infection.

Sequence identity: The similarity between nucleic acid or amino acid sequences is expressed in terms of the similarity between the sequences. Sequence identity is frequently measured in terms of percentage identity (or similarity or homology); the higher the percentage, the more similar the two sequences are. Homologs or variants of a protein or nucleic acid disclosed herein, such as target sequences associated with SEQ ID NOS: 1-232, and their corresponding cDNA and protein sequences, will possess a relatively high degree of sequence identity when aligned using standard methods.

Methods of alignment of sequences for comparison are well known in the art. Various programs and alignment algorithms are described in: Smith and Waterman, *Adv. Appl. Math.* 2:482, 1981; Needleman and Wunsch, *J. Mol. Biol.* 48:443, 1970; Pearson and Lipman, *Proc. Natl. Acad. Sci. U.S.A.* 85:2444, 1988; Higgins and Sharp, *Gene* 73:237-44, 1988; Higgins and Sharp, *CABIOS* 5:151-3, 1989; Corpet *et al.*, *Nucl. Acids Res.* 16:10881-90, 1988; Pearson and Lipman, *Proc. Natl. Acad. Sci. U.S.A.* 85:2444, 1988; and Altschul *et al.*, *Nature Genet.* 6:119-29, 1994:

The NCBI Basic Local Alignment Search Tool (BLAST<sup>TM</sup>) (Altschul *et al.*, *J. Mol. Biol.* 215:403-10, 1990) is available from several sources, including the National Center for Biotechnology Information (NCBI, Bethesda, MD) and on the Internet, for use in connection with the sequence analysis programs blastp, blastn, blastx, tblastn and tblastx.

Variants of a peptide, such as a peptide encoded by any target sequence associated with SEQ ID NOS: 1-227, 229, and 231, as well as any target sequence associated with SEQ ID NOS: 228, 230, and 232, are typically characterized by possession of at least 70% sequence identity counted over the full length alignment with the amino acid sequence encoded by any target sequence associated with SEQ ID NOS: 1-227, 229, or 231, using the NCBI Blast 2.0, gapped blastp set to default parameters. For comparisons of amino acid sequences of greater than about 30 amino acids, the Blast 2 sequences function is employed using the default BLOSUM62 matrix set to default parameters, (gap existence

cost of 11, and a per residue gap cost of 1). When aligning short peptides (fewer than around 30 amino acids), the alignment is performed using the Blast 2 sequences function, employing the PAM30 matrix set to default parameters (open gap 9, extension gap 1 penalties). Proteins with even greater similarity to the reference sequences will show increasing percentage identities when assessed by this method, such as at least 80%, at least 90%, at least 95%, at least 98%, or even at least 99% sequence identity. When less than the entire sequence is being compared for sequence identity, homologs and variants will typically possess at least 80% sequence identity over short windows of 10-20 amino acids, and may possess sequence identities of at least 85%, at least 90%, at least 95%, or at least 98% depending on their similarity to the reference sequence. Methods for determining sequence identity over such short windows are described at the website that is maintained by the National Center for Biotechnology Information in Bethesda, Maryland. One of skill in the art will appreciate that these sequence identity ranges are provided for guidance only; it is entirely possible that strongly significant homologs could be obtained that fall outside of the ranges provided.

Similar methods can be used to determine the sequence identity between two or more nucleic acids. To compare two nucleic acid sequences, the BLASTN options can be set as follows: -i is set to a file containing the first nucleic acid sequence to be compared (such as C:\seq1.txt); -j is set to a file containing the second nucleic acid sequence to be compared (such as C:\seq2.txt); -p is set to blastn; -o is set to any desired file name (such as C:\output.txt); -q is set to -1; -r is set to 2; and all other options are left at their default setting. For example, the following command can be used to generate an output file containing a comparison between two sequences: C:\BI2seq -i c:\seq1.txt -j c:\seq2.txt -p blastn -o c:\output.txt -q -1 -r 2.

Once aligned, the number of matches is determined by counting the number of positions where an identical nucleotide or amino acid residue is presented in both sequences. The percent sequence identity is determined by dividing the number of matches either by the length of the sequence set forth in the identified sequence, or by an articulated length (for example, 100 consecutive nucleotides or amino acid residues from a sequence set forth in an identified sequence), followed by multiplying the resulting value by 100. For example, a nucleic acid sequence that has 1166 matches when aligned with a test sequence having 1154 nucleotides is 75.0 percent identical to the test sequence (for example,  $1166 \div 1554 \times 100 = 75.0$ ). The percent sequence identity value is rounded to the nearest tenth. For example, 75.11, 75.12, 75.13, and 75.14 are rounded down to 75.1, while 75.15, 75.16, 75.17, 75.18, and 75.19 are rounded up to 75.2. The length value will always be an integer. In another example, a target sequence containing a 20-nucleotide region that aligns with 20 consecutive nucleotides from an identified sequence as follows contains a region that shares 75 percent sequence identity to that identified sequence (for example,  $15 \div 20 \times 100 = 75$ ).

		1		20
Target Sequence:		AGGTCGTGTACTGTCAGTCA		
Identified Sequence:		ACGTGGTGAAGTCCAGTGA		

The nucleic acids disclosed herein include nucleic acids have nucleotide sequences that are at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, or at least 99% identical to the nucleotide sequence of any target sequence associated with SEQ ID NOS: 1-227, 229, and 231. In particular examples, a nucleic acid is substantially similar to the nucleotide sequence of any target sequence associated with SEQ ID NOS: 1-227, 229, and 231. A first nucleic acid is "substantially similar" to a second nucleic acid if, when the first nucleic acid is optimally aligned (with appropriate nucleotide deletions or gap insertions) with the second nucleic acid (or its complementary strand) and there is nucleotide sequence identity of at least about 90%, for example at least about 95%, at least 98% or at least 99% identity. An alternative indication that two nucleic acid molecules are closely related is that the two molecules hybridize to each other under stringent conditions.

Nucleic acid sequences that do not show a high degree of identity may nevertheless encode similar amino acid sequences, due to the degeneracy of the genetic code. It is understood that changes in nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid molecules that all encode substantially the same protein.

**Short interfering or interrupting RNA (siRNA).** Double-stranded RNAs that can induce sequence-specific post-transcriptional gene silencing, thereby decreasing or even inhibiting gene expression. In some examples, siRNA molecules are about 19-23 nucleotides in length, such as at least 21 nucleotides, for example at least 23 nucleotides.

In one example, siRNA triggers the specific degradation of homologous RNA molecules, such as mRNAs, within the region of sequence identity between both the siRNA and the target RNA. For example, WO 02/44321 discloses siRNAs capable of sequence-specific degradation of target mRNAs when base-paired with 3' overhanging ends. The direction of dsRNA processing determines whether a sense or an antisense target RNA can be cleaved by the produced siRNA endonuclease complex. Thus, siRNAs can be used to modulate transcription, for example, by silencing genes, such as Rab9,  $\beta$ -chimerin, or combinations thereof. The effects of siRNAs have been demonstrated in cells from a variety of organisms, including *Drosophila*, *C. elegans*, insects, frogs, plants, fungi, mice and humans (for example, WO 02/44321; Gitlin *et al.*, *Nature* 418:430-4, 2002; Caplen *et al.*, *Proc. Natl. Acad. Sci.* 98:9742-9747, 2001; and Elbashir *et al.*, *Nature* 411:494-8, 2001).

In certain examples, siRNAs are directed against certain target genes, such as Rab9,  $\beta$ -chimerin, or combinations thereof, to confirm results of the gene-trap method used against the same nucleic acid sequence.

**Specific binding agent.** An agent that binds substantially only to a defined target. For example, a protein-specific binding agent binds substantially only the specified protein and a nucleic acid specific binding agent binds substantially only the specified nucleic acid.

As used herein, the term "protein [X] specific binding agent" includes anti-[X] protein antibodies (including polyclonal or monoclonal antibodies and functional fragments thereof) and other agents (such as soluble receptors) that bind substantially only to the [X] protein. In this context, [X] refers to any specific or designated protein, for instance  $\beta$ -chimerin, Rab9, or any protein listed in Table

1 or encoded by a target sequence associated with SEQ ID NOS: 1-227, 229, and 231 (including variants, fragments, and fusions thereof).

Anti-[X] protein antibodies can be produced using standard procedures such as those described in Harlow and Lane (*Using Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Press: Cold Spring Harbor, 1998). Antibodies can be polyclonal or monoclonal antibodies, humanized antibodies, Fab fragments, F(ab')<sub>2</sub> fragments, single chain antibodies, or chimeric antibodies. For example, polyclonal antibodies can be produced by immunizing a host animal by injection with polypeptides described herein, including the target sequences associated with SEQ ID NOS: 1-227, 229, 231 (or variants, fragments, or fusions thereof). The production of monoclonal antibodies can be accomplished by a variety of methods, such as the hybridoma technique (Kohler and Milstein, *Nature* 256:495-7, 1975), the human B-cell technique (Kosbor *et al.*, *Immunology Today* 4:72, 1983), or the EBV-hybridoma technique (Cole *et al.*, in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96, 1983). Additionally, chimeric antibodies can be produced (for example, see Morrison *et al.*, *J. Bacteriol.* 159:870, 1984; Neuberger *et al.*, *Nature* 312:604-8, 1984; and Takeda *et al.*, *Nature* 314:452-4, 1985), as well as single-chain antibodies (for example, see U.S. Pat. Nos. 5,476,786; 5,132,405; and 4,946,778).

The determination that a particular agent binds substantially only to the specified protein readily can be made by using or adapting routine procedures. For example, Western blotting can be used to determine that a given protein binding agent, such as an anti-[X] protein monoclonal antibody, binds substantially only to the [X] protein. Other assays include, but are not limited to, competitive and non-competitive homogenous and heterogeneous enzyme-linked immunosorbent assays (ELISA) as symmetrical or asymmetrical direct or indirect detection formats; "sandwich" immunoassays; immunodiffusion assays; in situ immunoassays (for example, using colloidal gold, enzyme or radioisotope labels); agglutination assays; complement fixing assays; immunoelectrophoretic assays; enzyme-linked immunospot assays (ELISPOT); radioallergosorbent tests (RAST); fluorescent tests, such as used in fluorescent microscopy and flow cytometry; Western, grid, dot or tissue blots; dip-stick assays; halogen assays; or antibody arrays (for example, see O'Meara and Tovey, *Clin. Rev. Allergy Immunol.*, 18:341-95, 2000; Sambrook *et al.*, 2001, Appendix 9; Simonnet and Guilloteau, in: *Methods of Immunological Analysis*, Masseyeff *et al.* (Eds.), VCH, New York, 1993, pp. 270-388).

A specific binding agent also can be labeled for direct detection (see Chapter 9, Harlow and Lane, *Antibodies: A Laboratory Manual*. 1988). Suitable labels include (but are not limited to) enzymes (such as alkaline phosphatase (AP) or horseradish peroxidase (HRP)), fluorescent labels, colorimetric labels, radioisotopes, chelating agents, dyes, colloidal gold, ligands (such as biotin), and chemiluminescent agents.

Shorter fragments of antibodies can also serve as specific binding agents. For instance, Fabs, Fvs, and single-chain Fvs (SCFvs) that bind to a specified protein would be specific binding agents. These antibody fragments include: (1) Fab, the fragment containing a monovalent antigen-binding fragment of an antibody molecule produced by digestion of whole antibody with the enzyme papain to yield an intact light chain and a portion of one heavy chain; (2) Fab', the fragment of an

antibody molecule obtained by treating whole antibody with pepsin, followed by reduction, to yield an intact light chain and a portion of the heavy chain; two Fab' fragments are obtained per antibody molecule; (3) (Fab')<sub>2</sub>, the fragment of the antibody obtained by treating whole antibody with the enzyme pepsin without subsequent reduction; (4) F(ab')<sub>2</sub>, a dimer of two Fab' fragments held together by two disulfide bonds; (5) Fv, a genetically engineered fragment containing the variable region of the light chain and the variable region of the heavy chain expressed as two chains; and (6) single chain antibody ("SCA"), a genetically engineered molecule containing the variable region of the light chain, the variable region of the heavy chain, linked by a suitable polypeptide linker as a genetically fused single chain molecule. Methods of making these fragments are routine. For example, construction of Fab expression libraries permits the rapid and easy identification of monoclonal Fab fragments with the desired specificity for a protein described herein.

Subject: Living multi-cellular vertebrate organisms, including human and veterinary subjects, such as cows, pigs, horses, dogs, cats, birds, reptiles, and fish.

Target sequences associated with SEQ ID NO: When used herein, this phrase refers to any nucleic acid sequence, amino acid sequence, or combination of nucleic acid and amino acid sequences, that are involved in viral infection, and therefore serve as targets for inhibiting viral infection, and which are or include a specified SEQ ID NO, are involved in the expression of the SEQ ID NO, or are peptide (including protein) sequences that are expressed by such specified SEQ ID NO. Although a target sequence may refer to a SEQ ID NO of a sequence obtained from a particular species, the target sequences also include homologues of the sequence from other related species, such as other mammals. For example, the phrase "target sequences associated with SEQ ID NO. X" can refer to the entire gene sequence of which the particular SEQ ID NO X is a part, the appropriate coding sequence, a promoter sequence associated with the gene, or the corresponding protein sequence, as well as variants, fragments, homologues, and fusions thereof that retain the activity of the native sequence.

For example, when using the phrase "sequences associated with SEQ ID NOS: 21-22," this term encompasses  $\beta$ -chimerin genomic sequences, endogenous promoter sequences that promote the expression of  $\beta$ -chimerin, coding sequences, and  $\beta$ -chimerin proteins, as well as variants, fragments homologues and fusions thereof that retain the activity of the native sequence. A particular cDNA sequence associated with SEQ ID NOS: 21-22 is provided in GenBank Accession No. NM\_004067, and a particular protein sequence associated with SEQ ID NOS: 21-22 is provided in NP\_004058.1.

The term "a GenBank Accession No. associated with SEQ ID NO. X" refers to a GenBank Accession No. that includes SEQ ID NO. X, or is a homolog of SEQ ID NO: X from another mammal, for example a human homolog. The GenBank Accession No. may, in some examples, also identify a coding sequence of an open reading frame, and the sequence of the protein encoded by SEQ ID NO. X.

Although sequences are provided herein that encode (or are included within sequences that encode) host proteins that are involved in viral infection, it should be understood that the ultimate goal is to interfere with the activity of the protein that has been identified to be involved in viral

pathogenesis. Such interference can be at either the level of the nucleic acid that encodes the protein (for example by reducing or otherwise disrupting expression of the protein), or at the level of the protein itself (for example by interfering with the activity of the protein, or its interaction with the virus). The disclosure of specific techniques for achieving these goals in particular species should not  
5 be interpreted to limit the method to these particular techniques, or to particular species in which the viral interaction is first identified. The identification of the viral interaction in one species indicates the importance of the interaction between the virus and the protein in that species, as well as the interaction of the virus with homologues of that protein in other species.

**Target sequence of a nucleic acid:** A portion of a nucleic acid that, upon hybridization to a  
10 therapeutically effective oligonucleotide or oligonucleotide analog, results in reduction or even inhibition of infection by an infectious agent. An antisense or a sense molecule can be used to target a portion of dsDNA, since either can interfere with the expression of that portion of the dsDNA. The antisense molecule can bind to the plus strand, and the sense molecule can bind to the minus strand. Thus, target sequences can be ssDNA, dsDNA, and RNA.

**Therapeutically active molecule:** An agent, such as a protein, antibody or nucleic acid,  
15 that can decrease expression of a host protein involved in viral infection (such as those listed in Table 1 or target sequences associated with any of SEQ ID NOS: 1-232, or can decrease an interaction between a host protein involved in viral infection and a viral protein, such as HIV, Ebola, or influenza A, as measured by clinical response (for example, a decrease in infection by a virus, such as an  
20 inhibition of infection). Therapeutically active agents also include organic or other chemical compounds that mimic the effects of the therapeutically effective peptide or nucleic acids.

**Therapeutically Effective Amount:** An amount of a pharmaceutical preparation that alone, or together with an additional therapeutic agent(s), induces the desired response. The preparations disclosed herein are administered in therapeutically effective amounts.

**In one example,** a desired response is to decrease or inhibit viral infection of a cell, such as a  
25 cell of a subject. Viral infection does not need to be completely inhibited for the pharmaceutical preparation to be effective. For example, a pharmaceutical preparation can decrease viral infection by a desired amount, for example by at least 20%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or even at least 100%, as compared to an amount of  
30 viral infection in the absence of the pharmaceutical preparation. This decrease or inhibition can result in halting or slowing the progression of, or inducing a regression of a pathological condition caused by the viral infection, or which is capable of relieving signs or symptoms caused by the condition.

**In another or additional example,** it is an amount sufficient to partially or completely  
alleviate symptoms of viral infection within a host subject. Treatment can involve only slowing the  
35 progression of the infection temporarily, but can also include halting or reversing the progression of the infection permanently.

Effective amounts of the therapeutic agents described herein can be determined in many different ways, such as assaying for a reduction in the rate of infection of cells or subjects, a reduction in the viral load within a host, improvement of physiological condition of an infected subject, or

increased resistance to infection following exposure to the virus. Effective amounts also can be determined through various *in vitro*, *in vivo* or *in situ* assays, including the assays described herein.

The disclosed therapeutic agents can be administered in a single dose, or in several doses, for example daily, during a course of treatment. However, the effective amount of can be dependent on the source applied (for example a nucleic acid isolated from a cellular extract versus a chemically synthesized and purified nucleic acid), the subject being treated, the severity and type of the condition being treated, and the manner of administration. In addition, the disclosed therapeutic agents can be administered alone, or in the presence of a pharmaceutically acceptable carrier, or in the presence of other therapeutic agents, for example other anti-viral agents.

10       **Transduced and Transformed:** A virus or vector "transduces" or "transfects" a cell when it transfers nucleic acid into the cell. A cell is "transformed" by a nucleic acid transduced into the cell when the DNA becomes stably replicated by the cell, either by incorporation of the nucleic acid into the cellular genome, or by episomal replication. As used herein, the term transformation encompasses all techniques by which a nucleic acid molecule might be introduced into such a cell, including transfection with viral vectors, transformation with plasmid vectors, and introduction of  
15       naked DNA by electroporation, lipofection, and particle gun acceleration.

**Transfected:** A transfected cell is a cell into which has been introduced a nucleic acid molecule by molecular biology techniques. The term transfection encompasses all techniques by which a nucleic acid molecule can be introduced into such a cell, including transfection with viral  
20       vectors, transformation with plasmid vectors, and introduction of naked DNA by electroporation, lipofection, and particle gun acceleration.

**Transgene:** An exogenous nucleic acid sequence supplied by a vector. In one example, a transgene includes any target sequence associated with SEQ ID NOS: 1-227, 229, 231 (or variants, fragments, or fusions thereof), for example a nucleic acid that encodes a beta-chimerin or Rab9.

25       **Variants, fragments or fusions:** The disclosed nucleic acid sequences, such as target sequences associated with SEQ ID NOS: 1-227, 229, and 231, and the proteins encoded thereby, include variants, fragments, and fusions thereof that retain the native biological activity (such as playing a role in viral infection). DNA sequences which encode for a protein or fusion thereof, or a fragment or variant of thereof can be engineered to allow the protein to be expressed in eukaryotic  
30       cells or organisms, bacteria, insects, and/or plants. To obtain expression, the DNA sequence can be altered and operably linked to other regulatory sequences. The final product, which contains the regulatory sequences and the therapeutic protein, is referred to as a vector. This vector can be introduced into eukaryotic, bacteria, insect, and/or plant cells. Once inside the cell the vector allows the protein to be produced.

35       One of ordinary skill in the art will appreciate that the DNA can be altered in numerous ways without affecting the biological activity of the encoded protein. For example, PCR can be used to produce variations in the DNA sequence which encodes a protein. Such variants can be variants optimized for codon preference in a host cell used to express the protein, or other sequence changes that facilitate expression.

**Vector:** A nucleic acid molecule as introduced into a host cell, thereby producing a transformed host cell. A vector can include nucleic acid sequences that permit it to replicate in a host cell, such as an origin of replication, and can also include one or more selectable marker genes and other genetic elements. An insertional vector is capable of inserting itself into a host nucleic acid.

5 For example, recombinant lambda-phage vectors of host genomes (Coffin *et al.*, *Retroviruses*, Chapter 5).

**Wild-type.** A naturally occurring, non-mutated version of a nucleic acid sequence. Among multiple alleles, the allele with the greatest frequency within the population is usually (but not necessarily) the wild-type. The term "native" can be used as a synonym for "wild-type."

10

### Nucleic Acids and Proteins Involved in Viral Infection

Examples of host nucleic acids and proteins that play a role in viral infection have been identified and are summarized in Table 1. These nucleic acids and proteins offer new targets for therapies that reduce or even inhibit or prevent viral infection, and offer new strategies for assessing the risk of infection among certain populations. While the target genes were identified in an assay using the recited virus, it is appreciated that infections agents such as viruses will share common pathways. Thus, the host sequences set forth below can be interfered with to decrease infection in a host cell.

20 Examples of viruses that can be inhibited are described in Virology, Volumes 1 and 2 by Bernard Fields, Second Edition, 1990, Raven Press. Exemplary viruses include, but are not limited to members of the family: Picornaviridae (such as Poliovirus, Coxsackievirus, Echovirus, Rhinovirus, and Hepatitis A and E); Calciviridae (such as Norwalk and related viruses); Togaviridae and Flaviviridae (such as hepatitis C, Alphavirus, and Rubella); Coronaviridae (such as SARS); Rhabdoviridae (such as Rabies); Filoviridae (such as Marburg and Ebola); Paramyxoviridae (such as Parainfluenza, Mumps, Measles, Hydra and Respiratory Syncytial virus); Orthomyxoviridae; 25 Bunyaviridae (including all subtypes and strains); Arenaviridae (such as lymphocytic choreomeningitis virus and lassa fever and related viruses); Reoviridae (such as Reovirus and Rotavirus); Retroviridae (such as HTLV, HIV, and Lentivirus); Papoviridae (such as Polyoma and Papilloma); Adenoviridae (such as Adenovirus); Parvoviridae (such as Parvovirus); Herpesviridae 30 (such as Herpes 1 and 2, Cytomegalovirus, Varicella-Zoster, Kaposi sarcoma related virus (HHV9), Epstein Barr Virus, and HHV6-7 (roseolavirus)); Poxviridae (such as Pox); Hepadnaviridae (such as Hepatitis B); as well as Hepatitis D virus, Hanta virus, and newly identified infectious agents.

Table 1: Examples of Host Genes and Proteins Implicated in Pathogenesis

Nucleic Acid or Protein	Associated Virus	SEQ ID NO:	GenBank Accession Nos for cDNA and Protein
T-cell receptor V beta chain	HIV	1-19	



T-cell receptor V-D-J beta 2.1 chain	HIV	20	
$\beta$ -chimerin (CHN2)	HIV	21-22	NM_004067; NP_004058.1
Malic enzyme 1 (ME1)	HIV and Influenza A	23	BC025246; AAH25246.1
Hypothetical protein XP_174419	HIV and Influenza A	24	
sequence from Chromosome 4q31.3-32	HIV and Influenza A	25-27	
alpha satellite DNA	HIV	28	
LOC253788 and LOC219938; coagulation factor III (F3) and LOC91759	HIV	29	
similar to KOX4 (LOC131880) and LOC166140	HIV	30	
LOC222474 and similar to Rho guanine nucleotide exchange factor 4, isoform a, APC-stimulated guanine nucleotide exchange factor (LOC221178); T-cell receptor beta	HIV	31	
ribosomal protein L7A-like 4 (RPL7AL4) and v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian) (SRC)	HIV	32	
KIAA0564	HIV	33	
alpha satellite DNA; M96 protein	HIV	34	
hypothetical protein similar to G proteins, especially RAP-2A (LOC57826); LOC161005 and osteoblast specific factor 2 (fasciclin I-like; OSF-2)	HIV	35	
Canis familiaris T-cell leukemia translocation-associated (TCTA) gene, aminomethyltransferase (AMT) gene, dystroglycan (DAG1) gene, and bassoon (BSN) gene	Influenza A	36-37	
LIM domain containing preferred translocation partner in lipoma (LPP)	Influenza A	38-48	
sequence between LOC253121 and hyaluronan synthase 2 (HAS2)	Influenza A	49	
Testin 2 and Testin 3 (TES)	Influenza A	50-57	
PTPN1 gene for protein tyrosine phosphatase, non-receptor type 1	Influenza A	58-59	
sequence between LOC149360 and LOC253961	Influenza A	60	
sequence between KIAA1560 and Tectorin beta (TECTB)	Influenza A	61	
Cadherin related 23 (CDH23)	Influenza A	62	BC032581; AAH32581.1 -
Myeloid/lymphoma or mixed lineage leukemia, translocated to 10 (MMLT10)	Influenza A	63	

exportin 5 (XPO5) and DNA polymerase eta (POLH)	Ebola	64-66	
heterogenous nuclear riboprotein C (C1/C2) (HNRPC)	Ebola	67-75	
alpha-endosulfine pseudogene (ENSAP) and LOC128741	Ebola	76	
LOC222888	Ebola	77	
LOC138421 and zinc finger protein 297B (ZNF297B)	Ebola	78	
sideroflexin 5 (SFXN5)	Ebola	79	AY044437; AAK95826
importin 9 (FLJ10402)	Ebola	80	
T-cell receptor beta	Ebola	81-82	
similar to murine putative transcription factor ZNF131 (LOC135952)	Ebola	83-99	
KIAA1259	Ebola	100-101	AB033085; NP_115572
MURR1 and CCT4	Ebola	102	
FLJ40773 and similar to ribosomal protein L24-like (LOC149360)	Ebola	103	
Testin 2 and 3 (TES)	Ebola	104-107	See above
polybromo 1 (PB1)	Ebola	108	NM_018165.2; NP_060635
DNA damage inducible transcript 3 (DDIT3) and KIAA1887	Ebola	109	
PDZ and LIM domain 1 (elfin) (PDLIM1)	Ebola	110	
LOC284803	Ebola	111-112	
PRO0097 and FLJ31958	Ebola	113	
small inducible cytokine E, member 1 (endothelial monocyte-activating) (SCYE1)	Ebola	114-116	
E3 ubiquitin ligase (SMURF2) and MGC40489	Ebola	117-119	
Ras oncogene family member Rab9	Ebola	118-119	
PRO1617 and retinoblastoma binding protein 1 (RBBP1)	Ebola	120-122	NM_000321; NP_000312.1
region of chromosome 2q12	Ebola	123	
elongation factor for selenoprotein translation	Ebola	124	NM_021937.1 NP_068756.1
Transcription factor SMIF (HSA275986)	Ebola	125-137	
KIAA1026	Ebola	138	
trinucleotide repeat containing 5 (TNRC5)	Ebola	139	
homogentisate 1,2-dioxygenase (HGD)	Ebola	140	
region of chromosome Xq23-24	Ebola	141	
region of chromosome 4p15.3	Ebola	142	
similar to LWamide neuropeptide precursor protein [Hydractinia echinata] (LOC129883)	Ebola	143	

region of chromosome 2q21	Ebola	144	
region of chromosome Xp11.4, including UPS9X	Ebola	145	
LOC221829	Ebola	146	
U3 small nuclear RNA	Ebola	147-154	
integrin, beta 1 (ITGB1)	Ebola	155-158	BC020057; AAH20057.1
acrosomal vesicle protein 1 (ACRV1) and CHK1 checkpoint homolog (CHEK1)	Ebola	159	
prospero-related homeobox 1 (PROX1)	Ebola	160	
FLJ20627 and FLJ12910	Ebola	161-173	
PIN2-interacting protein (PINX1) and SRY (sex-determining region Y)-box 7 (SOX7)	Ebola	174	
LOC131920	Ebola	175	
region of chromosome 13q14	Ebola	176	
neurotrophic tyrosine kinase, receptor, type 3 (NTRK3)	Ebola	177	
TERA protein and FLJ13224	Ebola	178-179	
LOC284260	Ebola	180	
POM (POM121 homolog) and ZP3 fusion (POMZP3)	Ebola	181-182	
DEAD/H box polypeptide 8 (DDX8) and similar to ribosomal protein L29 (cell surface heparin binding protein HIP) (LOC284064)	Ebola	183	
LOC345307 and UDP-N-acetyl-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNT7)	Ebola	184-186	
Mus musculus 5S rRNA pseudogene (Rn5s-ps1)	Ebola	187	
ribosomal protein L27a pseudogene (RPL27AP) and v-myb myeloblastosis viral oncogene homolog-like 2 (MYBL2)	Ebola	188-192	
Down's syndrome cell adhesion molecule like 1 (DSCAML1)	Ebola	193	
LOC148529	Ebola	194	
Huntingtin-associated protein interacting protein (HAPIP)	Ebola	195	NM_005338.4; NP_005329.3
LOC158525 and similar to RIKEN cDNA 1210001E11 (LOC347366)	Ebola	196-200	
hypothetical protein FLJ12910	Ebola	201-204	
LOC350411	Ebola	205	
allograft inflammatory factor 1 (AIF1) and HLA-B associated transcript 2 (BAT2)	Ebola	206	
C10orf7	Ebola	207	
LOC346658 and LOC340349	Ebola	208-209	
region of chromosome 12q21	Ebola	210	
LOC339248 and FLJ22659	Ebola	211	
SR rich protein DKFZp564B0769 and	Ebola	212	

hypothetical protein MGC14793			
FLJ10439	Ebola	213-214	NM_018093.1; NP_060563.1
cytochrome P450, family 11, subfamily A, polypeptide 1 (CYP11A1) and sema domain, immunoglobulin domain (Ig) and GPI membrane anchor, (semaphoring) 7A	Ebola	215-218	
ribosomal protein S16 (RPS16)	Ebola	219-220	BC004324.2; AAH04324.1
hypothetical protein DKFZp434H0115 and ATP citrate lyase (ACLY)	Ebola	221-222	
calnexin (CANX); protein tyrosine phosphatase, receptor type, K (PTPRK)	Ebola	223-224	
cyclin M2 (CNNM2)	Ebola	225	NM_017649.2; NP_060119.2
AXL receptor tyrosine kinase (AXL)	Ebola	226	BC032229; AAH32229.1
<i>Homo sapiens</i> chromosome 10 open reading frame 3	Ebola	227-228	
<i>Homo sapiens</i> chromosome 10 open reading frame 3 (C10orf3)	Ebola	229-230	
<i>Homo sapiens</i> fer-1-like 3, myoferlin ( <i>C. elegans</i> )	Ebola	231-232	NM_013451.; NP_038479.1

Some of the host nucleic acids described in Table 1 and target sequences associated with SEQ ID NOS: 1-227, 229, and 231 encode polypeptides that are receptors or ligands recognized by a particular virus, such as HIV, influenza A, or the Ebola virus. For example, the T-cell receptor V beta and V-D-J beta 2.1 chain polypeptides are part of the T-cell receptor complex that are recognized by certain glycoproteins in the HIV envelope. Other host nucleic acids encode polypeptides that provide an enzymatic function related to a viral life cycle, such as the signaling pathways controlling viral packaging or enzymes involved in viral replications. For example, the  $\beta$ -chimerin rho-GTPase may mediate a cellular signal that initiates or triggers a process leading to passage of an HIV viral particle into the host cell. The data presented herein indicate that Rab9 is involved in pathogen infectivity, for example by interfering with trafficking of proteins and lipids within cells. In particular examples, it is demonstrated that Rab9 is involved in lipid raft formation, and that decreasing functional Rab9 and lipid rafts decreases the ability of pathogens, such as viruses and bacteria, that hijack lipid rafts to bud or be infectious.

Still other host nucleic acids participate in the life cycle of a virus. For example, a certain nucleotide sequence of a host nucleic acid, such as a gene within the host genome can be recognized during insertion and integration of a viral genome (reverse transcribed into DNA from the viral RNA genomic template) into the host genome. Viral integration is described in, for example, Coffin *et al.*, *Retroviruses*, Chapter 5.

The nucleic acids and proteins disclosed herein can be identified, isolated, and characterized using any number of techniques of molecular biology, including the specific methods and protocols described herein, such as in the examples below. In some examples, the nucleic acids were identified

and isolated using the Lexicon Genetics, Inc. (The Woodlands, TX) "gene trap" technology disclosed in U.S. Pat. Nos: 6,080,576; 6,136,566; 6,207,371; 6,139,833; 6,218,123 and 6,448,000.

Gene trap technology is a powerful method for cloning and identifying functional genes, as it marks a gene with a tag and simultaneously generates a corresponding genetic variation for that particular locus. The method involves introducing into a cell a DNA construct that can monitor and potentially disrupt the transcriptional activity of the region of the cell's genome into which it is inserted. The gene-trap method used to identify the host sequences is disclosed in U.S. Patent No. 6,448,000 (herein incorporated by reference).

Briefly, the gene trap protocol involves infecting a host cell (for example, a cell of a Sup T-1 cell line (human), MDCK cells (canine), or Vero cells (monkey)) with a recombinant vector (for example, U3neoSV1, FIG. 1). The recombinant vector includes a selectable marker or other sequence capable of being used to select infected host cells. However, the selectable marker or other sequence does not have a promoter at its 5' end. An exemplary selectable marker is a nucleic acid encoding resistance to an antibiotic (such as neomycin). A summary of the gene trap method is provided in FIGS. 2 and 3. Infection of the host cell is performed in culture under conditions that yield about one copy of the vector per cell. The vector incorporates into the host cell genome adjacent to an active promoter and interrupts or disrupts the transcription of a nucleic acid in the host cell (FIG. 2). The host promoter drives expression of the selectable marker or other sequence on the vector, and infected cells can then be selected. For example, if the vector carries a nucleic acid encoding neomycin resistance, cells can be selected on a medium that contains neomycin or G418, the neomycin analog for mammalian cells, depending on the type of host cell used.

The selected host cells are expanded in culture to form a library of cells that contain randomly disrupted host genes (FIG. 3). An aliquot of the library of cells is exposed to the appropriate virus, such as HIV, influenza A, or Ebola, to determine the effect of the disrupted host sequence on viral infection of the host cells. Host cells that survive the viral infection, or are relatively resistant to such infection (such as those cells that survive for a longer period of time than about at least 50% of the infected cells), can include one or more disrupted genes involved in viral infection. Thus, by using the vector one can decrease viral or pathogenic infection of a host cell or in a subject. Therefore, by identifying these disrupted genes that decreased or otherwise interfered with viral infection of the host cell, candidate sequences are identified that can be used as targets to decrease or inhibit viral infection.

Those host cells that survive viral infection, or are relatively resistant to such infection, are cloned, for example, by limit dilution using a chambered plate or by growth on methylcellulose. The interrupted host nucleic acid is identified using standard molecular biology methods. For example, host DNA can be isolated from the cell and digested using an appropriate restriction enzyme to free the 5' and 3' sequences adjacent the incorporated vector. The isolated DNA fragment can then be amplified, for example using PCR or by introducing the DNA fragment into a bacterial host cell then growing the bacteria. Once isolated, the host nucleic acid can be further characterized and analyzed.

For example, the nucleic acid can be sequenced and compared to other similar nucleic acids. Methods of using these nucleic acids, and the proteins encoded thereby, are discussed below.

Using these gene trap methods, several host molecules were identified that were previously not known to be involved in viral pathogenesis (SEQ ID NOS: 1-232, Table 1, and target sequences associated with SEQ ID NOS: 1-232). For example, the AMT gene (target sequences associated with SEQ ID NOS: 36 and 37) participates in influenza A infection of host cells. Fragments of host sequences involved in viral infection and pathogenesis can now be identified, even including fragments or sequences that were previously known to be important in the pathogenesis of intracellular pathogens. For example, although the T-cell receptor was previously implicated in HIV infection, the results disclosed herein demonstrate that the T-cell receptor V-D-J beta 2.1 chain (target sequences associated with SEQ ID NO: 20) is involved and in some examples required for HIV infection, and host cells lacking the T-cell receptor V-D-J beta 2.1 chain are unexpectedly highly resistant to HIV infection. Hence the V-D-J beta 2.1 chain is a target for anti-viral therapy at the DNA or polypeptide level, and other pathogenically active subcomponents of other known pathogenic sequences can also be identified with this method.

Examples of these host nucleic acid molecules are target sequences associated with SEQ ID NOS: 1-227, 229, and 231 (including variants, fragments, and fusions thereof) and summarized in Table 1. In addition to these specifically disclosed nucleotide sequences, a host nucleic acid can include nucleotide sequences that are similar to any of the target sequences associated with SEQ ID NOS: 1-227, 229, and 231, such as having at least 70% identity, at least 80% identity, at least 85% identity, at least 90% identity, at least 95% identity, at least 98% identity, or even at least 99% identity to any of the target sequences associated with SEQ ID NOS: 1-227, 229, and 231. The disclosed host nucleic acid sequences, and methods of using them, may comprise, consist, or consist essentially of any of the disclosed nucleic acid sequences shown in SEQ ID NOS: 1-227, 229, and 231, as well as target sequences associated with SEQ ID NOS: 1-227, 229, and 231, or variants or fragments thereof, or sequences that hybridize to the identified sequences under stringent or moderately stringent conditions.

The host nucleic acid molecules also include a fragment of any target sequence associated with SEQ ID NOS: 1-227, 229, and 231, such as a probe or primer as described below.

Host polypeptides corresponding to these nucleic acids also can be used to practice the disclosed methods. In some examples, the polypeptide includes an amino acid sequence that corresponds to a coding sequence of any target sequence associated with SEQ ID NOS: 1-227, 229, and 231, or a target protein sequence associated with SEQ ID NOS: 228, 230, and 232. However, host polypeptides can also include those having similar amino acid sequences, such as polypeptides that are at least 70% identical, at least 80% identical, at least 90% identical, at least 95% identical, at least 98% identical, or at least 99% identical to the amino acid sequences corresponding to translations of the coding sequence of any target sequence associated with SEQ ID NOS: 1-227, 229, and 231, or a target protein sequence associated with SEQ ID NOS: 228, 230, and 232. For example, the disclosed host polypeptides and methods of using them, may comprise, consist, or consist

essentially of an amino acid sequence corresponding to a translation of the nucleotide sequence in any target sequence associated with SEQ ID NOS: 1-227, 229, and 231, a target protein sequence associated with SEQ ID NOS: 228, 230, and 232, or any of the protein sequences listed in Table 1. Alternatively, the polypeptides include homologous polypeptides from other mammals (for example  
5 human, monkeys, and dogs).

The host polypeptide can have an amino acid sequence that varies by one or more conservative substitutions from the amino acid sequences of the proteins encoded by target sequences associated with SEQ ID NOS: 1-227, 229, and 231, or from the target amino acid sequences associated with SEQ ID NOS: 228, 230, and 232. In one example, there is no more than 1, 2, 3, 4, 5,  
10 or 10 conservative amino acid substitutions. In another example, there are 1, 2, 3, 4, 5 or 10 conservative amino acid substitutions. The effects of these amino acid substitutions, deletions, or additions on host polypeptides can be assayed, for example, by analyzing the ability of cells transformed with the derivative proteins to resist infection by the corresponding virus.

Also included are fragments of any host polypeptide encoded by any of the target sequences  
15 associated with SEQ ID NOS: 1-227, 229, and 231, as well as fragments of the target amino acid sequences associated with SEQ ID NOS: 228, 230, and 232. For example, a protein can include at least 5-500 contiguous amino acids of the protein, such as at least 6-200, at least 6-100, at least 10-100, at least 10-50, or at least 20-50 contiguous amino acids of the protein. A host polypeptide fragment can be at least 5, at least 10, at least 15, at least 25, at least 50, at least 100, at least 200, at  
20 least 500, or more amino acids of a polypeptide having an amino acid sequence corresponding to a coding region of the nucleotide sequence in any of the target sequences associated with SEQ ID NOS: 1-227, 229, and 231, or a conservative variant thereof, as well as target amino acid sequences associated with SEQ ID NOS: 228, 230, and 232.

Fragments of a nucleic acid target sequences associated with SEQ ID NOS: 1-227, 229, and  
25 231 can include 10-5000 contiguous nucleic acids, such as 12-1000, 12-500, 15-100, or 18-50 contiguous nucleic acids. A host nucleic acid fragment can be at least at least 5, at least 10, at least 15, at least 20, at least 25, at least 50, at least 100, at least 200, at least 500, at least 1000, at least 2000, at least 5000 or more contiguous nucleic acids in any target sequence associated with SEQ ID NOS: 1-227, 229, and 231, or a variant or fusion thereof.

Also included are host nucleic acids that encode the same polypeptide encoded by any target  
30 sequence associated with SEQ ID NOS: 1-227, 229, and 231, or a conservative variant of the polypeptide, or a fragment thereof. For example, a host nucleic acid provided by target sequences associated with SEQ ID NOS: 36-37 encodes AMT. A second host nucleic acid also can encode an AMT having the same amino acid sequence as the AMT encoded by target sequences associated with  
35 SEQ ID NOS: 36-37, a conservative variant of this AMT, or a fragment thereof, yet this second host nucleic acid can have a different nucleotide sequence than a target sequence associated with SEQ ID NOS: 36-37 due to the degeneracy of the genetic code.

### Methods of Using Host Sequences to Decrease Viral Infection

The interaction between a host nucleic acid or polypeptide (such as target sequences associated with SEQ ID NOS: 1-232 and those shown in Table 1) and a virus or viral protein can be decreased or inhibited using the methods provided. Decreasing or inhibiting this interaction can be used to decrease viral infection of a host cell, and/or to decrease symptoms associated with a viral infection in a subject. For example, decreasing or even inhibiting the interaction of a host nucleic acid or polypeptide and a virus can decrease, inhibit, or even prevent infection of a host cell by that virus, or otherwise inhibit the progression or clinical manifestation of the viral infection. In addition, decreasing the interaction of a host nucleic acid or polypeptide and a virus can reduce or alleviate one or more symptoms associated with viral infection, such as a fever.

Several methods can be used to decrease or inhibit the interaction between a viral protein and a host protein or nucleic acid. The viral and host proteins or nucleic acids can be part of an *in vitro* solution, an *in vivo* expression system, or *in situ* with a host tissue or subject. The viral protein can be part of a larger molecule or complex, such as an envelope protein on the envelope of a mature virus or a fragment of a viral envelope. The host protein also can be part of a larger molecule or complex, such as a host polypeptide expressed as part of a fusion protein or contained as one subunit of a larger protein, such as a transport protein, cell receptor, structural protein, or an enzyme. A host nucleic acid can be part of a larger molecule, complex, organism or microorganism such as a host nucleic acid contained within its host genome, a recombinant vector, or a transgenic organism or microorganism (including both extrachromosomal molecules or genomic insertions).

In accordance with the disclosed methods, interaction is decreased or inhibited between a virus or viral protein and more than one (such as 2 or more, such as 3 or more) host nucleic acids or polypeptides. Decreasing or inhibiting the interactions of one or more host nucleic acids or polypeptides with one or more viral proteins can have additive or exponentially increasing effects. For example, it is believed that decreasing the interaction between a host T-cell receptor V-D-J beta 2.1 chain and HIV, or decreasing the activity of a host  $\beta$ -chimerin, within a host cell can enhance the inhibitory effect on HIV infection of that host cell compared to inhibiting the interaction of only one of the host polypeptides. Hence, the methods include interfering with an interaction between the virus or viral protein and more than one of the proteins associated with infection by the same virus.

For example, for infection with HIV, the method could interfere with one, or two or more (such as three or more) of the following: T-cell receptor V beta chain; T-cell receptor V-D-J beta 2.1 chain;  $\beta$ -chimerin (CHN2); malic enzyme 1; Hypothetical protein XP\_174419; sequence from Chromosome 4q31.3-32; alpha satellite DNA; LOC253788; LOC219938; coagulation factor III (F3); LOC91759; similar to KOX4 (LOC131880); LOC166140; LOC222474; similar to Rho guanine nucleotide exchange factor 4, isoform a; APC-stimulated guanine nucleotide exchange factor (LOC221178); T-cell receptor beta; ribosomal protein L7A-like 4 (RPL7AL4); v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian) (SRC); KIAA0564; alpha satellite DNA; M96 protein; hypothetical protein similar to G proteins (such as RAP-2A; LOC57826); LOC161005 and osteoblast specific factor 2 (fasciclin I-like).



For Ebola virus, examples of targets include one, or two or more (such as three or more) of the following: exportin 5; DNA polymerase eta (POLH); heterogeneous nuclear riboprotein C (C1/C2); alpha-endosulfine pseudogene; LOC128741; LOC222888; LOC138421; zinc finger protein 297B; sideroflexin 5; importin 9; T-cell receptor beta; similar to murine putative transcription factor ZNF131 (LOC135952); KIAA1259; MURR1; CCT4; FLJ40773 and similar to ribosomal protein L24-like (LOC149360); testin 2; testin 3; polybromo 1; DNA damage inducible transcript 3 (DDIT3); KIAA1887; PDZ and LIM domain 1 (elfin) (PDLIM1); LOC284803; PRO0097 and FLJ31958; small inducible cytokine E, member 1 (endothelial monocyte-activating); E3 ubiquitin ligase (SMURF2) and MGC40489; Rab9; PRO1617 and retinoblastoma binding protein 1 (RBBP1); region of chromosome 2q12; elongation factor for selenoprotein translation; transcription factor SMIF (HSA275986); KIAA1026; trinucleotide repeat containing 5; homogentisate 1,2-dioxygenase; region of chromosome Xq23-24; region of chromosome 4p15.3; similar to LWamide neuropeptide precursor protein [Hydractinia echinata] (LOC129883); region of chromosome 2q21; region of chromosome Xp11.4, including UPS9X; LOC221829; U3 small nuclear RNA; integrin, beta 1; acrosomal vesicle protein 1 (ACRV1) and CHK1 checkpoint homolog (CHEK1); prospero-related homeobox 1 (PROX1); FLJ20627 and FLJ12910; PIN2-interacting protein (PINX1) and SRY (sex-determining region Y)-box 7 (SOX7); LOC131920; region of chromosome 13q14; neurotrophic tyrosine kinase, receptor, type 3 (NTRK3); TERA protein; FLJ13224; LOC284260; POM (POM121 homolog) and ZP3 fusion (POMZP3); DEAD/H box polypeptide 8 (DDX8) and similar to ribosomal protein L29 (cell surface heparin binding protein HIP) (LOC284064); LOC345307 and UDP-N-acetyl-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNT7); 5S rRNA pseudogene; ribosomal protein L27a pseudogene (RPL27AP) and v-myb myeloblastosis viral oncogene homolog-like 2 (MYBL2); Down's syndrome cell adhesion molecule like 1; LOC148529; Huntingtin-associated protein interacting protein; LOC158525 and similar to RIKEN cDNA 1210001E11 (LOC347366); hypothetical protein FLJ12910; LOC350411; allograft inflammatory factor 1 (AIF1); HLA-B associated transcript 2 (BAT2); C10orf7; LOC346658; LOC340349; region of chromosome 12q21; LOC339248; FLJ22659; SR rich protein DKFZp564B0769; hypothetical protein MGC14793; FLJ10439; cytochrome P450, family 11, subfamily A, polypeptide 1; sema domain, immunoglobulin domain (Ig) and GPI membrane anchor, (semaphoring) 7A; ribosomal protein S16; hypothetical protein DKFZp434H0115; ATP citrate lyase; calnexin; protein tyrosine phosphatase, receptor type, K (PTPRK); cyclin M2; AXL receptor tyrosine kinase; *Homo sapiens* chromosome 10 open reading frame 3, mRNA (cDNA clone MGC:3422 IMAGE:3028566); *Homo sapiens* chromosome 10 open reading frame 3, (C10orf3); and *Homo sapiens* fer-1-like 3, myoferlin (*C. elegans*) (FER1L3), transcript variant 1.

For influenza, examples of targets include one, or two or more (such as three or more) of the following: T-cell leukemia translocation-associated (TCTA) gene, aminomethyltransferase; dystroglycan; BSN; LIM domain containing preferred translocation partner in lipoma (LPP); sequence between LOC253121 and hyaluronan synthase 2 (HAS2); testin 2; testin 3; PTPN1 gene for protein tyrosine phosphatase, non-receptor type 1; sequence between LOC149360 and LOC253961;

sequence between KIAA1560 and tectorin beta; cadherin related 23; myeloid/lymphoma or mixed lineage leukemia, translocated to 10; malic enzyme 1; hypothetical protein XP\_174419; and sequence from chromosome 4q31.3-32.

5 In examples where a host polypeptide is a cell receptor or part of a cell receptor, decreasing or preventing expression of the polypeptide, or altering the three-dimensional structure of the polypeptide, can reduce or inhibit the interaction between the host cell receptor and a viral protein. Similarly, decreasing, inhibiting or preventing expression of a host ligand polypeptide (or altering the structure of such a ligand) can decrease or inhibit an interaction between the viral protein and the ligand. For example, decreasing or inhibiting expression of one or more enzymes involved in viral  
10 pathogenesis, such as those listed in Table 1 and those target sequences associated with SEQ ID NOS: 1-232, can block a component of the viral life cycle, such as blocking a signal pathway leading to transcription or translation of the viral genome, or assembly of viral sub-parts. Decreasing or inhibiting the enzymatic activity of an enzyme (rather than its expression) can have a similar effect.

15 Altering the nucleotide sequence of a host nucleic acid, for example by targeting disruption of the nucleotide sequence using complementary nucleic acid sequences, can decrease, inhibit or prevent integration of a viral nucleic acid into the host nucleic acid. Methods that can be used to interrupt or alter translation of a host nucleic acid include, but are not limited to, using an antisense RNA, RNAi molecule, or an siRNA that binds to a messenger RNA transcribed by the nucleic acid encoding a host polypeptide as described herein. Decreasing or inhibiting the expression of the host  
20 nucleic acid can also alter the course of the disease. In one example, altering the nucleotide sequence of a host gene that is targeted by a virus for viral integration can decrease, inhibit, or even prevent, integration of that virus into the host genome.

A host nucleic acid involved in viral infection, including variants, fusions and fragments thereof, can be used to design agents that bind to a target sequence of that nucleic acid, such as  
25 antisense nucleic acids or siRNAs. Such nucleic acid binding agents can be used to decrease or inhibit expression of the nucleic acid, to reduce the incidence of viral infection. For example, an expression vector that transcribes antisense RNA or siRNA that recognizes human  $\beta$ -chimerin mRNA is used to transform cell lines obtained from simians. These transformed cell lines are analyzed for infection by simian immunodeficiency virus (SIV), which is related to HIV. If those cells are  
30 resistant to SIV infection, the disrupted gene is identified, sequenced, and compared to the human  $\beta$ -chimerin gene. Sequence similarities between the two genes will offer insight into common molecular mechanisms for infection by HIV and SIV, for example, common structural regions within their respective translated proteins.

A binding agent that recognizes a host nucleic acid involved in viral infection can be used  
35 for prophylactic or therapeutic purposes. For example, expression vectors having antisense RNA, RNAi molecules, or siRNA molecules that target a host nucleic acid involved in viral infection, such as  $\beta$ -chimerin, are introduced into the bone marrow of a subject. Uptake of the vector and expression of the antisense RNA, RNAi, or siRNA within cells infected by HIV offers a prophylactic or therapeutic effect by disrupting the  $\beta$ -chimerin genes within those cells, thus decreasing or inhibiting

HIV infection. Similarly, expression vectors including Rab9 antisense RNA, RNAi, or siRNA molecules can be introduced into the bone marrow of a subject. Uptake of the vector and expression of Rab9 antisense RNA, RNAi, or siRNA within cells infected by a pathogen that can hijack a lipid raft, such as HIV or Ebola, offers a prophylactic or therapeutic effect by disrupting the Rab9 genes within those cells, thus decreasing or even inhibiting infection by a pathogen that can hijack a lipid raft. The vector, or other nucleic acid carrying the nucleic acid specific binding agent, is introduced into a subject by any standard molecular biology method and can be included in a composition containing a pharmaceutically acceptable carrier.

Decreasing or inhibiting the interaction between a viral protein and a host protein can decrease or inhibit viral infection. Methods that can be used to decrease an interaction between a viral protein and one or more host proteins (such as at least 2 host proteins, or at least 3 host proteins), include but are not limited to, disrupting expression of a host nucleic acid sequence encoding the host protein, (for example by functionally deleting the coding sequence, such as by a mutation, insertion, or deletion), altering the amino acid sequence or overall shape of the host protein, degrading the host protein, employing an agent that interferes with the viral protein or host protein (such as a specific binding agent, for example an antibody or small molecule), or a combination thereof.

For example, expression of a host protein can occur during transcription or translation of a nucleic acid encoding the host protein, or as a result of post-translational modification of a host protein. Methods that can be used to interrupt or alter transcription of a nucleic acid include, but are not limited to, site-directed mutagenesis, including mutations caused by a transposon or an insertional vector; and providing a DNA-binding protein that binds to the coding region of the host protein, thus blocking or interfering with RNA polymerase or another protein involved in transcription. Various inactive and recombinant DNA-binding proteins, and their effects on transcription, are discussed in Lewin, *Genes VII*. Methods that can be used to interrupt or alter translation of a nucleic acid include, but are not limited to, using an antisense RNA or an siRNA that binds to a messenger RNA transcribed by the nucleic acid encoding the host polypeptide as described herein.

For example, exemplary host T-cell receptor polypeptides are encoded by target sequences associated with SEQ ID NOS: 1-20. Disrupting the expression of a nucleic acid including any target sequence associated with SEQ ID NOS: 1-20 can reduce or prevent production of the corresponding T-cell receptor polypeptide, and without access to the T-cell receptor polypeptide, an HIV virus cannot infect the host cell. Even if expression of the host nucleic acid is not completely blocked or disrupted, virus infection can still be inhibited. For example, interference with a host protein encoded by any target sequence associated with SEQ ID NOS: 1-20 reduces the number of T-cell receptors within that host cell available for recognition by an HIV virus, thus inhibiting HIV infection.

It is shown herein that inhibiting the interaction or activity between host Rab9 and HIV and Ebola using Rab9 siRNA molecules decreases infection of a host cell by the virus compared to the amount of infection in the absence of the siRNA molecules.

Host proteins involved in viral infection, such as those encoded by target cDNA sequences associated with SEQ ID NOS: 1-227, 229, and 231, as well as target sequences associated with SEQ ID NOS: 228, 230, and 232, can be used to generate specific binding agents to those proteins. The specific binding agent can be an anti-protein binding agent, such as a monoclonal or polyclonal antibody. Anti-protein binding agents can provide a prophylactic or therapeutic effect, for example by interfering with viral infection. Assays to determine whether an antibody interferes with viral infection are described herein. Antibodies that recognize a host protein involved in viral infection can prevent a virus or portion thereof (such as a viral protein) from binding to a host protein involved in viral infection. For example, a monoclonal or polyclonal antibody that binds to a V beta T-cell receptor on a cell can block the binding of HIV to that T-cell receptor, thus blocking infection of that cell. Effective amounts of such specific binding agents can be administered alone to a subject, or as part of a pharmaceutical composition, for the treatment of viral infection or as a prophylactic measure prior to the time the subject is exposed to the virus. In another example, specific binding agents that recognize a host protein involved in viral infection, such as  $\beta$ -chimerin or Rab9, can be used can be used to screen for the presence of the host protein, in other cells, tissues or lysates, including a biological sample obtained from a subject.

Host nucleic acids and polypeptides described herein, such as target sequences associated with SEQ ID NOS: 1-232, can be used for prophylactic or therapeutic uses. For example, polypeptides with structures mimicking a protein recognized by a virus can be administered to a subject as a pharmaceutical composition. These polypeptides interact with a virus already infecting that subject, or provide a prophylactic defense mechanism against infection if the subject is at risk of exposure to a virus. For example, polypeptides structurally similar to the T-cell receptor V beta 2.1 chain are recognized by HIV. If such polypeptides are administered to an HIV-positive subject, the viruses already present in the subject interact with those polypeptides in addition to that subject's T-cell receptors, thus inhibiting the rate at which HIV infects T-cells. The administered polypeptides act as "decoys" to block HIV from interacting with T-cell receptors. As another example, an agent that otherwise interferes with the interaction between a virus and a host protein can provide a similar prophylactic effect. For example, a chemical compound or anti-AMT binding agent (such as an antibody) that interferes with the interaction between AMT and an influenza virus (including an enzymatic inhibitor of AMT) provides a prophylactic or therapeutic effect against influenza A infection when provided to a host cell or administered to a host subject.

Additionally, the proteins described herein can be used to screen samples for the presence or absence of a particular antibody. For example, a  $\beta$ -chimerin or Rab9 protein can be used in an ELISA to screen a sample obtained from an individual for the presence of anti- $\beta$ -chimerin or anti-Rab9 antibodies generated by that individual, such as a blood sample.

Using a method similar to that described for nucleic acid binding agents above, protein binding agents (such as agents that specifically bind  $\beta$ -chimerin, Rab9, or V beta T-cell receptor proteins) can be used to screen cells, individuals or populations for the presence or absence of

polypeptides related to infection (such as HIV, Ebola, or influenza infection), thus providing information about the susceptibility or resistance of that individual or population to viral infection.

The host nucleic acids, proteins, and related specific binding agents described herein can be used as models for the design of anti-viral drugs. For example, the three-dimensional structure of a protein described herein, such as  $\beta$ -chimerin, can be used in computer modeling of chemotherapeutic agents that block the activity of that moiety, for example by binding the protein. As another example, a monoclonal antibody can be used in a competitive binding assay to screen for other compounds that bind the same antigen.

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### Screening for Resistance to Infection

Also provided herein are methods of screening host subjects for resistance to infection by characterizing a nucleotide sequence of a host nucleic acid or the amino acid sequence of a host polypeptide (such as those shown in Table 1, or any target sequence associated with SEQ ID NOS: 1-232).

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For example, the T-cell receptor V beta 2.1 chain nucleic acid of a subject can be isolated, sequenced, and compared to SEQ ID NO: 20 (or a target sequence associated with SEQ ID NO: 20). The greater the similarity between that subject's V beta 2.1 chain nucleic acid and the sequence shown in SEQ ID NO: 20 (or a target sequence associated with SEQ ID NO: 20), the more susceptible that person is to HIV infection, while a decrease in similarity between that subject's V beta 2.1 chain nucleic acid and SEQ ID NO: 20 (or a target sequence associated with SEQ ID NO: 20), the more resistant that subject can be to HIV infection.

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In another example, the aminomethyltransferase (AMT) nucleic acid of a subject can be isolated, sequenced, and compared to SEQ ID NOS: 36-37 (or a target sequence associated with SEQ ID NOS: 36-37). The greater the similarity between that subject's AMT nucleic acid and the sequence shown in SEQ ID NOS: 36-37 (or a target sequence associated with SEQ ID NOS: 36-37), the more susceptible that person is to influenza A infection, while a decrease in similarity between that subject's AMT nucleic acid and SEQ ID NOS: 36-37 (or a target sequence associated with SEQ ID NOS: 36-37), the more resistant that subject can be to influenza A infection.

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In yet another example, the Ras oncogene family member Rab9 nucleic acid of a subject can be isolated, sequenced, and compared to SEQ ID NOS: 118-119 (or a target sequence associated with SEQ ID NOS: 118-119). The greater the similarity between that subject's Rab9 nucleic acid and the sequence shown in SEQ ID NOS: 118-119 (or a target sequence associated with SEQ ID NOS: 118-119), the more susceptible that person is to infection by a pathogen that uses lipid rafts, such as those listed in Table 2, while a decrease in similarity between that subject's Rab9 nucleic acid and SEQ ID NOS: 118-119 (or a target sequence associated with SEQ ID NOS: 118-119), the more resistant that subject may be to infection by a pathogen that uses lipid rafts.

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Assessing the genetic characteristics of a population can provide information about the susceptibility or resistance of that population to viral infection. For example, polymorphic analysis of AMT alleles in a particular human population, such as the population of a particular city or

geographic area, can indicate how susceptible that population is to influenza A infection. A higher percentage of AMT alleles substantially similar to SEQ ID NOS: 36-37 (or a target sequence associated with SEQ ID NOS: 36-37) indicates that the population is more susceptible to influenza A infection, while a large number of polymorphic alleles that are substantially different than SEQ ID NOS: 36-37 (or a target sequence associated with SEQ ID NOS: 36-37) indicates that a population is more resistant to influenza A infection. Such information can be used, for example, in making public health decisions about vaccinating susceptible populations.

#### Transgenic Cells and Non-Human Mammals

Transgenic animal models, including recombinant and knock-out animals, can be generated from the host nucleic acids described herein. Exemplary transgenic non-human mammals include, but are not limited to, mice, rats, chickens, cows, and pigs. In certain examples, a transgenic non-human mammal has a knock-out of one or more of the target sequences associated with SEQ ID NOS: 1-35, and has a decreased viral susceptibility, for example infection by HIV. In certain embodiments, a transgenic non-human mammal has a knock-out of any of the target sequences associated with SEQ ID NOS: 36-63, and has a decreased viral susceptibility, for example infection by influenza A. In certain examples, a transgenic non-human mammal has a knock-out of any of the target sequences associated with SEQ ID NOS: 64-232, and has a decreased viral susceptibility, for example infection by Ebola. In certain examples, a transgenic non-human mammal has a knock-out of any target sequence associated with SEQ ID NOS: 118-119, and has a decreased susceptibility to infection by a pathogen that uses a lipid raft, such as those listed in Table 2. Such knock-out animals are useful for reducing the transmission of viruses from animals to humans. In addition, animal viruses that utilize the same targets provided herein can be decreased in the animals.

Expression of the sequence used to knock-out or functionally delete the desired gene can be regulated by choosing the appropriate promoter sequence. For example, constitutive promoters can be used to ensure that the functionally deleted gene is never expressed by the animal. In contrast, an inducible promoter can be used to control when the transgenic animal does or does not express the gene of interest. Exemplary inducible promoters include tissue-specific promoters and promoters responsive or unresponsive to a particular stimulus (such as light, oxygen, chemical concentration, such as a tetracycline inducible promoter).

For example, a transgenic mouse including an AMT gene (such as a target sequence associated with SEQ ID NOS: 36-37), or a mouse having a disrupted AMT gene, can be examined during exposure to various mammalian viruses related to influenza A. Comparison data can provide insight into the life cycles of influenza and related viruses. Moreover, knock-out animals (such as pigs) that are otherwise susceptible to an infection (for example influenza) can be made to determine the resistance to infection conferred by disruption of the gene.

Transgenic pigs having a disrupted human protein tyrosine phosphatase gene can be produced and used as an animal model to determine other types of infections, including viral infections in mammals related to influenza A. A transgenic pig resistant to infection by viruses other

than influenza A is used to demonstrate the relatedness of influenza and those other viruses.

Transgenic animals, including methods of making and using transgenic animals, are described in various patents and publication, such as WO 01/43540; WO 02/19811; U.S. Pub. Nos: 2001-0044937 and 2002-0066117; and U.S. Pat. Nos: 5,859,308; 6,281,408; and 6,376,743; and the references cited therein.

Cells including an altered or disrupted host nucleic acid or polypeptide having a role in viral infection (such as a target sequence associated with SEQ ID NOS: 1-232), are resistant to infection by a virus (see Example 2). Such cells may therefore include cells having decreased susceptibility to HIV infection (such as cells having altered or disrupted target sequence associated with SEQ ID NOS: 1-35), Ebola infection (such as cells having altered or disrupted target sequence associated with SEQ ID NOS: 64-232), or influenza A (such as cells having altered or disrupted target sequence associated with SEQ ID NOS: 36-63). For example, cells in which a  $\beta$ -chimerin gene was disrupted using the gene-trap method remain CD4<sup>+</sup> after HIV infection and do not produce further detectable HIV virus particles. Thus, disrupting the expression of  $\beta$ -chimerin can confer resistance on the cell to infection by HIV. Additionally, interfering with the activity of  $\beta$ -chimerin, such as contacting a  $\beta$ -chimerin with an enzymatic inhibitor or an anti- $\beta$ -chimerin binding agent, can confer a similar resistance to HIV infection.

#### Screening for Agents that Decrease Viral Infection

A host nucleic acid or polypeptide involved in viral infection, such as a target sequence associated with SEQ ID NOS: 1-232, and peptides listed in Table 1, can be used to identify agents that inhibit the binding of a virus or viral protein to a host nucleic acid, a host protein, or another target protein capable of binding to the virus or viral protein. In some examples, a host molecule, such as a host protein or nucleic acid is contacted with a viral molecule, such as a virus or portion thereof, for example as a viral protein. One or more test agents are contacted with the host molecule, the viral molecule, both both molecules, before, during or after contacting the host and viral molecules. Subsequently, it is determined whether binding of the viral molecule to the host molecule is decreased in the presence of the test agent, wherein a decrease in binding is an indication that the test agent decreases the binding of viral protein to the target protein.

In other examples, a cell-based assay is used to identify proteins that decrease viral infection, for example using the yeast two-hybrid system.

For example, the binding of the T-cell receptor V-D-J beta 2.1 chain polypeptide to HIV (or an HIV envelope glycoprotein) can be determined in the presence of a test agent. A decrease in binding activity between the T-cell receptor V-D-J beta 2.1 chain polypeptide and HIV indicates that the test agent decreases the binding of HIV to the T-cell receptor V-D-J beta 2.1 chain, and the agent is a candidate for use as an anti-HIV agent. A decrease in binding activity can be determined by a comparison to a reference standard, such as a binding activity reported in the scientific literature, or to a control. Any suitable compound or composition can be used as a test agent, such as organic or inorganic chemicals, including aromatics, fatty acids, and carbohydrates; peptides, including

monoclonal antibodies, polyclonal antibodies, and other specific binding agents; or nucleic acids.

The virus or viral molecule can be obtained from any suitable virus, such as HIV, influenza A, Ebola, and related viruses.

Therapeutic agents identified with the disclosed approaches can be used as lead compounds to identify other agents having even greater antiviral activity. For example, chemical analogs of identified chemical entities, or variant, fragments of fusions of peptide agents, are tested for their ability to decrease viral infection using the disclosed assays. Candidate agents are also tested for safety in animals and then used for clinical trials in animals or humans.

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#### Microarrays

The host nucleic acids or proteins disclosed herein having a role in viral infection, such as a target sequence associated with SEQ ID NOS: 1-232, can be used in an array. The array can be a microarray, such as a nucleic acid array that includes probes to different polymorphic alleles of a human AMT gene (for example target sequence associated with SEQ ID NOS: 36-37) or a human Rab9 gene (for example target sequence associated with SEQ ID NOS: 118-119). Kits can be generated, such as diagnostic kits or kits for screening for the presence or absence of a host nucleic acid within a biological sample obtained from a subject or kits for administering an effective amount of a specific binding agent to a subject for a therapeutic or prophylactic purpose.

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The following examples are provided to illustrate particular features of certain embodiments, but the scope of the claims should not be limited to those features exemplified.

#### Example 1

##### Generation of Cells with Increased Resistance to Viral Infection

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The gene-trap method was used to identify cellular genes needed for viral propagation but whose inactivation is not lethal to the host cell. This was accomplished by using a Moloney murine leukemia virus-derived shuttle vector that encodes for a promoterless neomycin-resistance gene (FIG. 1). This vector integrates into the host genome at transcriptionally active genes, thereby disrupting the host gene but utilizing the host promoter to drive neomycin resistance carried by the vector. The cells are then infected with the desired virus. Cells surviving the viral infection carry an interrupted host gene that is needed during the viral life cycle. Since the construct is a shuttle vector, it can function as a plasmid and can be moved from mammalian to bacterial systems, facilitating subcloning and DNA sequencing. Using this approach, loci involved in, and in some cases required for viral infection, for example by HIV-1 and HIV-2, influenza A and Ebola virus were identified.

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##### *Tissue culture*

Sup-T1 human lymphoblastic leukemia cells were cultured in RPMI-1640 medium supplemented with 10% heat-inactivated fetal-calf serum (FCS), penicillin, streptomycin and Fungisome. MDCK normal canine kidney-cells were cultured in DMEM supplemented with 10%



fetal bovine serum (FBS), penicillin, streptomycin. Vero African green monkey kidney cells were cultured in DMEM supplemented with 10% FBS, amphotericin B, streptomycin, and Glutamine. All cultures were grown under 5% CO<sub>2</sub>. Selection by all media was done in the presence of either 1 mg/ml (Sup-T1 and MDCK cells) or 400 mg/ml G418 (Geneticin; Vero cells).

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#### *Generation of gene-trapped library of cells*

Parental, virus sensitive cells were plated and infected with U3neoSV1 as follows.

Retrovirus vectors were obtained from H. Earl Ruley (Department of Microbiology and Immunology, Vanderbilt University School of Medicine, Nashville, TN). Stocks of the U3neoSV1 virus were prepared as described (Chen *et al.*, Gene trap retroviruses in *Methods in Molecular Genetics* (1994), page 123, herein incorporated by reference).

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FIG. 1 illustrates the U3neoSV1 retroviral vector, which contains a promoterless neomycin phosphotransferase gene (*Neo<sup>R</sup>*) within the U3 unique sequence of the 5' long terminal repeat (LTR) of MMLV. Additionally, a second mutationally inactivated copy of *neo* is present in the 3' LTR.

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Portions of the MMLV genome were removed to impair replication, and were replaced with the  $\beta$ -lactamase gene which confers ampicillin resistance (*Amp<sup>R</sup>*) to *E. coli* as well as an *E. coli* origin of replication (*ori*), flanked by two unique restriction sites for *Bam*HI (position 2570) and *Eco*RI (position 4175). Sites and orientations of primers used for sequence analysis of cloned genomic fragments are indicated by the triangular arrowheads.

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Parental, virus sensitive cells (106 Sup-T1 for HIV, Madin-Darby canine kidney, (MDCK) for influenza A, or Vero cells for Ebola) were plated for 12 hours before infection, after which U3neoSV1 was added at a multiplicity of infection (MOI) of 0.1, as titered by adding 1 ml of diluted stocks to cultured cells in the presence of 4  $\mu$ g/ml polybrene. The cells were incubated at 37°C for one hour, 10 ml of fresh medium added, and the cells were incubated overnight at 37°C. The next day, the medium was replaced with the appropriate media containing 1 mg/ml G418 and maintained until surviving cells approached confluence, which was usually about two weeks.

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Upon random integration of the U3neoSV1 vector into the host genome, endogenous promoters result in expression of *Neo<sup>R</sup>*, while expression of the exons 3' to the site of integration is disrupted. Therefore, only those events occurring at transcriptionally active promoters of non-essential genes are selected.

30

A pool of the surviving cells, termed a library, including many cells bearing different disrupted genes was then exposed to the pathogen of interest. The resulting Sup-T1 library cells, MDCK library cells, and Vero library cells were infected HIV-1 and HIV-2; the A/PR/8/34 virus reassortant having A/Johannesburg/82/96 glycoproteins (H1N1); and Ebola, respectively, as follows.

35

An aliquot of the cell library was infected with three rounds of HIV-1 and three rounds of HIV-2 (3Bx in BC7 cells), normally a lethal event for Sup T-1 cells (FIG. 4). Approximately  $3 \times 10^8$  actively growing Sup-T1 library cells were infected with the CXCR4 cytopathic HIV-1 strain LAI at an MOI of 10, approximately 100 fold greater than that normally used for spreading infection in culture. The cells were incubated with the virus for four hours in 2 ml of medium, then grown in bulk

at  $10^6$  cells/ml for two weeks, at which time G418 was added to a final concentration of 1 mg/ml and the cultures continued for an additional two weeks. The surviving cells were exposed to two further rounds of HIV-1 infection as described above and shown in FIG. 4.

Following HIV-1 infection, surviving cells were incubated 1:100 with BC7 T cells constitutively expressing the HIV-2 strain 3BX, which was modified to infect regardless of CD4 status, solely using the CXCR4 receptor. Cells were cocultured for two weeks followed by selection with 1 mg/ml G418 (same as FIG. 4, but with HIV-2 instead of HIV-1). The surviving cells were exposed to two further rounds of HIV-2 infection.

The final cell culture was selected using anti-CD4 magnetic microbeads (Miltyni) and divided into 2.0 ml cultures containing 1000 cells each. These were then infected with LAI at an MOI of 10. Surviving cells from each culture were subjected to limit dilution, or growth on methylcellulose, and expanded in selection medium. The isolated clones were identified as being CD4 and CXCR4 positive following flow cytometry analysis using standard protocols. Several cell isolates were resistant to further HIV infection with unique expression of CD4 cell surface antigen.

For influenza infection, approximately  $10^7$  actively growing MDCK library cells were washed with phosphate buffered saline (Gibco) and infected with the A/PR/8/34 virus reassortant having A/Johannesburg/82/96 glycoproteins (H1N1) at an MOI of 20-30 in 250  $\mu$ l DMEM in a T-25 flask. The cells were incubated with the virus for two hours, and the inoculum was subsequently replaced with DMEM, supplemented with 2% FBS and 1  $\mu$ g/ml TPCK trypsin (to cleavage-activate HA of new progeny virus). The cells were incubated for 18 hours to provide 2-3 rounds of infection. The maintenance medium was removed and replaced with selection medium (DMEM with 10% FBS and 1 mg/ml neomycin) and survivors allowed to expand. The surviving cells were exposed to one additional round of infection as described.

For filovirus infection, vero library cells were infected with either the Gulu 2000 or Zaire 1976 Ebola (EBO) strains, or the Voegelé 1967 strain of Marburg (MBG) at an MOI of greater than one in T-75 flasks in medium supplemented with 400 mg/ml G418. After a cytopathic effect (CPE) of 4+ was attained (greater than one week), survivors were harvested and reseeded undiluted and at 1:16 and 1:256 dilutions in selection medium. Wells with growth after 10 or more days were reinoculated into T12.5 flasks in selection medium and allowed to expand.

Cells surviving Ebola or influenza infection were cloned by either limiting dilution or growth on methylcellulose. The isolates were characterized phenotypically by flow cytometry and the interrupted gene determined by inverse PCR, cloning into BAC, or by the use of the shuttle feature of the vector followed by DNA sequence analysis.

## Example 2

### Cloning and Sequencing of Trapped Genes

This example describes the methods used to clone the sequences conferring resistance to the library of cells surviving viral infection. The identified sequences (SEQ ID NOS: 1-227, 229, 231)

encode host proteins that are involved in pathogen infection, and in some cases are required for the infectivity by the pathogen.

#### *Isolation of trapped genes*

5 The genomic DNA from actively growing virus-resistant isolates was extracted, prepared, and electroporated into cells as follows. Cellular DNA from actively growing virus-resistant isolates was extracted from one million cells using the QIAamp DNA Blood Mini Kit (Qiagen, Inc.) according to the manufacturer's instructions. Genomic DNA was digested at a final concentration of 150 µg/ml with either *EcoRI* or *BamHI* (New England Biolabs) at 1.5 or 2 units/µl, respectively (see 10 FIG. 1). Digested DNA was ethanol precipitated using oyster glycogen (Sigma) as a carrier, resuspended to a final concentration of 60 ng/µl and ligated using T4 DNA ligase (New England Biolabs). Genomic digestion resulted in the fragmentation of the retrovirus and the genomic DNA. Ligations were subsequently ethanol precipitated in the presence of glycogen, resuspended in 3 µl water and used directly to transform *E. coli*.

15 A 1.5 µl aliquot of each precipitated ligation was added to thawed Genehog cells (Invitrogen) or SURE cells (Stratagene), electroporated using a GenePulser (BioRad) according to the manufacturer's instructions, and plated onto Luria broth (LB) agar (1% tryptone, 0.5% yeast extract, 0.5% NaCl, 2% agar) containing 100 µg/µl carbenicillin (Sigma). Clones were isolated after 24 hours and used to inoculate 3 ml LB containing 100 µg/µl carbenicillin. Plasmid DNA was prepared after 20 overnight growth using the QIAprep Spin Miniprep Kit (QIAGEN, Inc.) according to the manufacturer's instructions and eluted in water.

#### *Sequencing of Shuttle Clones*

25 Due to the position of the unique sites in U3neoSV1, *BamHI* digestion facilitates cloning of DNA 3' to the site of integration, while *EcoRI* digestion results in the cloning of genomic DNA 5' to the site of integration. Using oligonucleotides homologous to the U3neoSV1 fragment, the sequence of the disrupted genomic DNA flanking the gene-trap insertion site was determined as follows.

Sequencing reactions were performed using the ABI BigDye terminator cycle sequencing kit with reaction products resolved on either an ABI 3100 Genetic Analyzer or an ABI 377 DNA 30 Sequencer (Applied Biosystems, Foster City, CA). Sequences were obtained by using oligonucleotides 5'-ATCTTGTTCATCATGCG (SEQ ID NO: 235) and 5'-GGGTCTGACGCTCATG (SEQ ID NO: 236) for *EcoRI*-generated shuttle clones, or 5'-GATAGGTGCCTCACTG (SEQ ID NO: 237) for *BamHI*-generated shuttle clones.

#### *Sequence analysis*

35 Sequences obtained from shuttle clones were analyzed by the Repeatmasker Web Server, available on the Internet at the website for the Department of Molecular Biotechnology, University of Washington, followed by standard nucleotide-nucleotide BLAST (blastn) against the National Center for Biotechnology Information databases, including nr (non-redundant

GenBank+EMBL+DDBJ+PDB sequences), est (expressed sequence tags) and htgs (unfinished High Throughput Genomic Sequences: phases 0, 1 and 2). Additionally, a nucleotide-protein database (blastx) analysis was performed against the nr database.

### 5 *Candidate Host Genes Required for Pathogenesis*

Candidate host genes required for the indicated pathogen, which were cloned via the gene-trap method and sequenced, are presented in Table 1 and in SEQ ID NOS: 1-226. The CD4<sup>+</sup>, latently infected, noninfectious HIV-resistant isolates 18B, 18E, 2B, and 2E were used to recover the genes involved in HIV-1 and HIV-2 pathogenesis, influenza A-resistant isolates B1, B3, B5, B6, and B7 were used to recover the host genes involved in influenza A pathogenesis, and Ebola-resistant isolates ZV and MV were used to recover the host genes involved in Ebola pathogenesis. Candidate genes can be validated by siRNA and cDNA complementation, as described in Example 3.

In summary, using the U3neoSV1 gene-trap, sixteen HIV-1 and -2 resistant Sup-T1 cell lines, and fifteen influenza A resistant MDCK cell lines were isolated and characterized. Twenty-three EBO-Zaire resistant Vero cell line pools, twenty-four EBO-Gulu resistant pools, and thirty MBG resistant pools were screened. The shuttle-vector design of the U3neoSV1 gene-trap allowed identification of multiple host genes involved in the pathogenesis of HIV-1, HIV-2, influenza A, and Ebola, which are described herein and summarized in Table 1 and sequences provided in SEQ ID NOS: 1-232. Cross-resistance of resistant isolates to multiple pathogens can be quickly examined to reveal common pathways in the viral life cycles.

### Example 3

#### siRNA Molecules Decrease Viral Infection

This example describes methods used to express siRNAs that recognize Rab9 (such as a target sequence associated with SEQ ID NOS: 118-119), AXL (AXL receptor tyrosine kinase; such as a target sequence associated with SEQ ID NO: 226), CHN (beta-chimerin; such as a target sequence associated with SEQ ID NOS: 21-22), KOX (such as a target sequence associated with SEQ ID NO: 30), RBB (retinoblastoma binding protein 1; such as a target sequence associated with SEQ ID NOS: 120-122), KIAA1259; F3 (such as a target sequence associated with SEQ ID NO: 29), and Mselb (mammalian selenium binding protein; such as a target sequence associated with SEQ ID NO: 124).

The following Rab9 siRNA sequences were generated by Dharmacon, RNA Technologies (Lafayette, CO) using chemical synthesis: GGGAAGAGTTCACCTTATGA (SEQ ID NO: 238); TCACAAAGCTTCCAGAACT (SEQ ID NO: 239); GTAACAAGATTGACATAAG (SEQ ID NO: 240); and GGAAGTGGATGGACATTTT (SEQ ID NO: 241).

The following AXL (AXL receptor tyrosine kinase) siRNA sequences were generated by Dharmacon, RNA Technologies using chemical synthesis: GGUCAGAGCGUGGAGGAUUU (SEQ ID NO: 242); GAAAGAAGGAGACCCGUUA (SEQ ID NO: 243);

CCAAGAAGAUCUACAAUGG (SEQ ID NO: 244); and GGAACUGCAUGCUGAAUGA (SEQ ID NO: 245).

5 siRNA sequences were also used that recognized CHN (beta-chimerin); KOX (similar to KOX4 (LOC131880) and LOC166140); RBB (retinoblastoma binding protein 1); KIAA1259; F3 and mammalian selenium binding protein. One skilled in the art will understand that siRNA sequences that recognize other sequences involved in viral infection (such as a target sequence associated with any of SEQ ID NOS: 1-232) can be designed and prepared by commercial entities, such as Dharmacon, RNA Technologies.

10 The four siRNA sequences for each gene (CHN, KOX, RBB, RAB, KIAA1259, F3, ASL and Mselb) were separately pooled. Each of the eight pools of siRNAs, hybridized to its appropriate complement sequence, were used to transfect JCS3 (HeLa cells modified to accept HIV), Vero (monkey kidney cells), MDCK (dog kidney cells), or HEK (human kidney cells). All cells were obtained from American Type Culture Collection (ATCC, Manassas, VA). GFP siRNA sequences were used as a negative control.

15 Cells (20,000 to 250,000) were incubated in serum free media for 24 hours. Cocktails were made by mixing the appropriate duplex siRNAs (50-100 pmoles) with lipofectamine 2000 (4-16 µl) and RNase Inhibitor (1-4 µl) in a solution of OptiMem (serum free medium) in a total volume of 200-2000 µl. The lipofectamine was allowed to incubate at room temperature for 5 minutes before the addition of siRNA. Aliquots (50-500 µl) of the cocktail were added to the cells which were 20 incubated at 37°C for 48 hours. The cells were then infected with HIV, Ebola, or influenza and the incubation continued for 3-7 days. Following transfection, several assays were conducted to confirm transfection efficiency, and to determine the resistance of the cells to infection by various agents.

Quantitation of p24 levels in HIV infected JCS3 cells was determined using the Coulter HIV-1 p24 Antigen Neutralization Kit according to the manufacturers recommendation. As shown in 25 FIG. 5, Rab9 siRNAs and mammalian selenium binding protein siRNAs each decreased HIV infection by about 50% on day 4 post infection (day 7 post addition of siRNA). In addition, HIV infection decreased by about 80-90% in the presence of beta-chimerin siRNAs, KOX (similar to KOX4 (LOC131880) and LOC166140) siRNAs, or retinoblastoma binding protein 1 siRNAs. However, HIV infection did not decrease in the presence of siRNAs that recognize KIAA1259, tissue 30 factor 3, or AXL receptor tyrosine kinase. It is possible that apoptosis is interrupted by the siRNAs, so the cell lives through the infection but still makes virus. It is also possible that the p24 levels are elevated but is not associated with infectious particles.

To determine the level of Ebola infection in HEK293-cells transfected with Rab9 or AXL siRNA, the presence of gp1 antigen was determined by using a fluorescent antibody to gp1 envelope 35 protein. Infection by Ebola decreased by at least about 90-95% in the presence of Rab9 siRNA, as compared to the amount of infection in the absence of Rab9 siRNA. Infection by Ebola decreased by at least about 80% in the presence of AXL siRNA, as compared to the amount of infection in the absence of AXL siRNA.

## Example 4

## Expression of Rab9 siRNA Decreases Lipid Raft Formation

As described in Example 3, siRNA molecules that recognize Rab9 decrease viral infection. Rab9 transports late endosomes to trans-golgi. Based on these results, a model is proposed whereby Rab9 plays a role in lipid raft formation (FIG. 6). Lipid rafts are liquid-ordered microdomains enriched in sphingolipids and cholesterol, and are involved in biosynthetic traffic, signal transduction, and endocytosis. Viruses take advantage of ("hijack") rafts for completion of some steps of their replication cycle, such as entry into their cell host, assembly, and budding. Without wishing to be bound to a particular theory, it is proposed that Rab9 trafficks cholesterol, the dynamic glue that holds lipid rafts together. Further evidence for this hypothesis is based on observations of Neimann-Pick type C disease cells. Neimann-Pick type C is a genetic disease that results in accumulation of abnormally high levels of intracellular cholesterol. However, over expression of Rab9 in Neimann-Pick type C disease cells, decreases the level of cholesterol.

Examples of pathogens that hijack lipid rafts include, but are not limited to those shown in Table 2. In the absence of functional Rab9 and lipid rafts (or a decrease in the number of rafts), viruses may not be able to bud or be infectious. Therefore, the use of agents that decrease or inhibit Rab9 expression or activity can be used to decrease infection by other pathogens, as well as toxins such as anthrax, that hijack lipid rafts, such as those shown in Table 2.

Table 2: Pathogens that hijack lipid rafts.

Bacteria		Viruses	Protozoa
Intracellular survival	Toxin binding/oligomerization		
<i>Campylobacter jejuni</i>	<i>Vibrio cholerae</i>	SV40	<i>Toxoplasma gondii</i>
<i>Legionella pneumophila</i>	<i>Aeromonas hydrophila</i>	Echovirus 1 and 11	<i>Plasmodium falciparum</i>
<i>Brucella spp.</i>	<i>Clostridium spp.</i>	Avian sarcoma and leukosis virus	
<i>FimH</i> and <i>Dr Escherichia coli</i>	<i>Streptococcus pyogenes</i>	Semliki forest virus	
<i>Salmonella typhimurium</i>	<i>Bacillus anthracis</i>	Ecotropic mouse leukaemia virus	
<i>Shigella flexneri</i>	<i>Bacillus thuringiensis</i>	HTLV-1	
<i>Chlamydia spp.</i>	<i>Helicobacter pylori</i>	HIV-1	
<i>Mycobacterium spp.</i>	<i>Lysteria monocytogenes</i>	Ebola and Marburg viruses	
		Measles virus	
		Herpes Simplex virus	
		Influenza virus	
		Epstein-Barr virus	

This example therefore illustrates that identification of an agent (such as a small molecule or siRNA) that inhibits a particular pathogen can be used to inhibit other pathogens that have a similar mechanism of action.

### Example 5

#### RNAi Molecules

This example describes methods that can be used to decrease or inhibit expression of any of the genes listed in Table 1, or target sequences associated with SEQ ID NOS: 1-232, to decrease viral infection, such as infection by HIV, Ebola, or influenza. Exemplary RNAi compounds are provided for several different genes, such as beta-chimerin receptor tyrosine kinase, retinoblastoma binding protein 1, *Homo sapiens* chromosome 10 open reading frame 3, *Homo sapiens* fer-1-like 3, myoferlin (*C. elegans*), transcript variant 1, *Homo sapiens* chromosome 10 open reading frame 3 (C10orf3), malic enzyme, cadherin related 23, sideroflexin 5, polybromo 1, elongation factor for selenoprotein translation, integrin, beta 1, huntingtin interacting protein 1 and cyclin M2.

One skilled in the art will understand that RNAi molecules can be generated to any of the genes listed in Table 1. Although only 27mers are shown in SEQ ID NOS: 246-845, this disclosure is not limited to RNAi compounds of a particular length. An RNAi molecule can be any length, such as at least about 25 nucleotides, or even as many as 400 nucleotides. One skilled in the art will also understand that RNAi sequences that recognize other sequences involved in viral infection (such as a target sequence associated with any of SEQ ID NOS: 1-232) can be designed and prepared by commercial entities, such as Sequitur, Inc. (Natick, MA).

Using the methods described in Example 3, the disclosed RNAi compounds are used to decrease viral infection. For example, a 27mer RNAi compound shown in any of SEQ ID NOS: 246-845 is incubated with its reverse complement, allowing hybridization of the two molecules. In particular examples, two or more, such as three or more, 27mer RNAi compounds are transfected into a cell. This duplex molecule is contacted with a cell, such as a cell of a subject in whom decreased viral infection is desired, under conditions that allow the duplex to enter the cell.

25

### Example 6

#### Disruption of Gene Expression

This example describes methods that can be used to disrupt expression of a host gene, such as those shown in Table 1 and target sequences associated with SEQ ID NOS: 1-232, and thereby decrease activity of the proteins encoded by these sequences. Such methods are useful when it is desired to decrease or inhibit viral infection. In a particular example, disrupted expression of at least one target sequence associated with SEQ ID NOS: 1-232 in a host cell is used to treat a subject having a viral infection, or susceptible to a viral infection. Methods useful for disrupting gene function or expression are the use of antisense oligonucleotides, siRNA molecules (see Example 3), RNAi molecules (see Example 5), ribozymes, and triple helix molecules. Techniques for the production and use of such molecules are well known to those of skill in the art.

35

#### Antisense Methods

To design antisense oligonucleotides, a host mRNA sequence is examined. Regions of the sequence containing multiple repeats, such as TTTTTTTT, are not as desirable because they will lack specificity. Several different regions can be chosen. Of those, oligos are selected by the following characteristics: those having the best conformation in solution; those optimized for hybridization characteristics; and those having less potential to form secondary structures. Antisense molecules having a propensity to generate secondary structures are less desirable.

Plasmids including antisense sequences that recognize one or more of the target sequences associated with SEQ ID NOS: 1-232 (such as a sequence that encodes a protein listed in Table 1) can be generated using standard methods. For example, cDNA fragments or variants coding for a host protein involved in viral infection are PCR amplified. The nucleotides are amplified using Pfu DNA polymerase (Stratagene) and cloned in antisense orientation a vector, such as pcDNA vectors (Invitrogen, Carlsbad, CA). The nucleotide sequence and orientation of the insert can be confirmed by sequencing using a Sequenase kit (Amersham Pharmacia Biotech).

Generally, the term "antisense" refers to a nucleic acid capable of hybridizing to a portion of a host RNA sequence (such as mRNA) by virtue of some sequence complementarity. The antisense nucleic acids disclosed herein can be oligonucleotides that are double-stranded or single-stranded, RNA or DNA or a modification or derivative thereof, which can be directly administered to a cell, or which can be produced intracellularly by transcription of exogenous, introduced sequences.

Antisense nucleic acids are polynucleotides, and can be oligonucleotides (ranging from about 6 to about 100 oligonucleotides). In one example, an antisense polynucleotide recognizes one or more of the target nucleic acid sequences associated with SEQ ID NOS: 1-227, 229, or 231. In specific examples, the oligonucleotide is at least 10, 15, or 100 nucleotides, or a polynucleotide of at least 200 nucleotides. However, antisense nucleic acids can be much longer. The nucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone, and can include other appending groups such as peptides, or agents facilitating transport across the cell membrane (Letsinger *et al.*, *Proc. Natl. Acad. Sci. USA* 1989, 86:6553-6; Lemaitre *et al.*, *Proc. Natl. Acad. Sci. USA* 1987, 84:648-52; WO 88/09810) or blood-brain barrier (WO 89/10134), hybridization triggered cleavage agents (Krol *et al.*, *BioTechniques* 1988, 6:958-76) or intercalating agents (Zon, *Pharm. Res.* 5:539-49, 1988).

An antisense polynucleotide (including oligonucleotides) that recognizes one or more of the target sequences associated with SEQ ID NOS: 1-227, 229, or 231, can be modified at any position on its structure with substituents generally known in the art. For example, a modified base moiety can be 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N-6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-



oxyacetic acid, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-S-oxyacetic acid, 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, and 2,6-diaminopurine.

5 An antisense polynucleotide that recognizes one or more of the target sequences associated with SEQ ID NOS: 1-227, 229, or 231, can include at least one modified sugar moiety such as arabinose, 2-fluoroarabinose, xylose, and hexose, or a modified component of the phosphate backbone, such as phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, or a formacetal or analog thereof.

10 In a particular example, an antisense polynucleotide that recognizes one or more of the target sequences associated with SEQ ID NOS: 1-227, 229, or 231 is an  $\alpha$ -anomeric oligonucleotide. An  $\alpha$ -anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual  $\beta$ -units, the strands run parallel to each other (Gautier *et al.*, *Nucl. Acids Res.* 15:6625-41, 1987). The oligonucleotide can be conjugated to another molecule, such as a  
15 peptide, hybridization triggered cross-linking agent, transport agent, or hybridization-triggered cleavage agent. Oligonucleotides can include a targeting moiety that enhances uptake of the molecule by host cells. The targeting moiety can be a specific binding molecule, such as an antibody or fragment thereof that recognizes a molecule present on the surface of the host cell.

Polynucleotides disclosed herein can be synthesized by standard methods, for example by  
20 use of an automated DNA synthesizer. As examples, phosphorothioate oligos can be synthesized by the method of Stein *et al.* (*Nucl. Acids Res.* 1998, 16:3209), methylphosphonate oligos can be prepared by use of controlled pore glass polymer supports (Sarin *et al.*, *Proc. Natl. Acad. Sci. USA* 85:7448-51, 1988). In a specific example, antisense oligonucleotide that recognizes one or more of the target sequences associated with SEQ ID NOS: 1-227, 229, or 231 includes catalytic RNA, or a  
25 ribozyme (see WO 90/11364, Sarver *et al.*, *Science* 247:1222-5, 1990). In another example, the oligonucleotide is a 2'-O-methylribonucleotide (Inoue *et al.*, *Nucl. Acids Res.* 15:6131-48, 1987), or a chimeric RNA-DNA analogue (Inoue *et al.*, *FEBS Lett.* 215:327-30, 1987).

The antisense polynucleic acids disclosed herein include a sequence complementary to at least a portion of an RNA transcript of a gene, such as a target sequence associated with SEQ ID  
30 NOS: 1-227, 229, or 231. However, absolute complementarity, although advantageous, is not required. A sequence can be complementary to at least a portion of an RNA, meaning a sequence having sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation can be assayed. The ability to hybridize depends on the degree of  
35 complementarity and the length of the antisense nucleic acid. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an RNA it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

The relative ability of polynucleotides (such as oligonucleotides) to bind to complementary strands is compared by determining the  $T_m$  of a hybridization complex of the poly/oligonucleotide and its complementary strand. The higher the  $T_m$  the greater the strength of the binding of the hybridized strands. As close to optimal fidelity of base pairing as possible achieves optimal hybridization of a poly/oligonucleotide to its target RNA.

The amount of antisense nucleic acid that is effective in the treatment of a particular disease or condition (the therapeutically effective amount) depends on the nature of the disease or condition, and can be determined by standard clinical techniques. For example, it can be useful to use compositions to achieve sustained release of an antisense nucleic acid, for example an antisense molecule that recognizes one or more target sequences associated with SEQ ID NOS: 1-227, 229, or 231. In another example, it may be desirable to utilize liposomes targeted via antibodies to specific cells.

As an alternative to antisense inhibitors, catalytic nucleic acid compounds, such as ribozymes or anti-sense conjugates, can be used to inhibit gene expression. Ribozymes can be synthesized and administered to the subject, or can be encoded on an expression vector, from which the ribozyme is synthesized in the targeted cell (as in WO 9523225, and Beigelman *et al. Nucl. Acids Res.* 1995, 23:4434-42). Examples of oligonucleotides with catalytic activity are described in WO 9506764. Conjugates of antisense with a metal complex, such as terpyridylCu (II), capable of mediating mRNA hydrolysis, are described in Bashkin *et al. (Appl. Biochem Biotechnol.* 54:43-56, 1995).

### *Ribozymes*

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. The mechanism of ribozyme action involves sequence specific hybridization of the ribozyme molecule to complementary target RNA, followed by an endonucleolytic cleavage. Methods of using ribozymes to decrease or inhibit RNA expression are known in the art. An overview of ribozymes and methods of their use is provided in Kashani-Sabet (*J. Investig. Dermatol. Symp. Proc.*, 7:76-78, 2002).

Ribozyme molecules include one or more sequences complementary to the target host mRNA and include the well-known catalytic sequence responsible for mRNA cleavage (see U.S. Pat. No. 5,093,246, herein incorporated by reference).

A ribozyme gene directed against any of the target sequences associated with SEQ ID NOS: 1-227, 229, or 231 can be delivered to a subject endogenously (where the ribozyme coding gene is transcribed intracellularly) or exogenously (where the ribozymes are introduced into a cell, for example by transfection). Methods describing endogenous and exogenous delivery are provided in Marschall *et al. (Cell Mol. Neurobiol.* 14:523-38, 1994).

Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the target molecule for ribozyme cleavage sites that include the following sequence: GUA, GUU and GUC. Once identified, short RNA sequences of between 15 and ribonucleotides

corresponding to the region of the target gene containing the cleavage site may be evaluated for predicted structural features, such as secondary structure, that may render the oligonucleotide sequence unsuitable. The suitability of candidate targets may also be evaluated by testing their accessibility to hybridization with complementary oligonucleotides, using ribonuclease protection assays.

For example, a plasmid that contains a ribozyme gene directed against a  $\beta$ -chimerin rho-GTPase, placed behind a promoter, can be transfected into the cells of a subject, for example a subject susceptible to HIV infection. Expression of this plasmid in a cell will decrease or inhibit  $\beta$ -chimerin rho-GTPase RNA expression in the cell. In another example, a plasmid that contains a ribozyme gene directed against Rab9 placed behind a promoter, can be transfected into the cells of a subject, for example a subject susceptible to infection by a pathogen that utilizes lipid rafts, such as Ebola. Expression of this plasmid in a cell will decrease or inhibit Rab9 RNA expression in the cell. Other examples of using ribozymes to decrease or inhibit RNA expression can be found in WO 01/83754 (herein incorporated by reference).

#### *Triple helix molecules*

Nucleic acid molecules used in triplex helix formation should be single stranded and composed of deoxynucleotides. The base composition of these oligonucleotides is ideally designed to promote triple helix formation via Hoogsteen base pairing rules, which generally require sizeable stretches of either purines or pyrimidines to be present on one strand of a duplex. Nucleotide sequences may be pyrimidine-based, which will result in TAT and CGC+ triplets across the three associated strands of the resulting triple helix. The pyrimidine-rich molecules provide base complementarity to a purine-rich region of a single strand of the duplex in a parallel orientation to that strand. In addition, nucleic acid molecules may be chosen that are purine-rich, for example, contain a stretch of guanidine residues. These molecules will form a triple helix with a DNA duplex that is rich in GC pairs, in which the majority of the purine residues are located on a single strand of the targeted duplex, resulting in GGC triplets across the three strands in the triplex.

Alternatively, the potential sequences that can be targeted for triple helix formation may be increased by creating a so called "switchback" nucleic acid molecule. Switchback molecules are synthesized in an alternating 5'-3', 3'-5' manner, such that they base pair with one strand of a duplex first and then the other, eliminating the necessity for a sizeable stretch of either purines or pyrimidines to be present on one strand of a duplex.

#### **Example 7**

##### **Methods of Treatment**

When the activity of a host cell protein or nucleic acid involved in viral infection is decreased by prematurely downregulating their levels of expressing using antisense molecules, a reduction in viral infection can be achieved. Antisense oligonucleotides, RNAi molecules, ribozymes, and siRNA molecules that recognize a host nucleic acid involved in viral infection

(Example 6) can therefore be used to disrupt cellular expression of a host protein involved in viral infection. The disclosed antisense, ribozyme, RNAi molecules and siRNA molecules can be administered to a subject alone, or in combination with other therapeutic agents such as anti-viral compounds.

5 A subject susceptible to or suffering from a viral infection, wherein decreased amounts of infection by the virus is desired, can be treated with a therapeutically effective amount of antisense, ribozyme, RNAi molecule or siRNA molecule (or combinations thereof) that recognizes a host sequence involved in viral infection, such as those shown in Table 1 or target sequences associated with SEQ ID NOS: 1-232. After the antisense, ribozyme, RNAi molecule or siRNA molecule has  
10 produced an effect (a decreased level of viral infection is observed, or symptoms associated with viral infection decrease), for example after 24-48 hours, the subject can be monitored for diseases associated with viral infection.

Similarly, other agents, such as an antibody that recognizes a host protein involved in viral infection and prevents the protein from interacting with a viral protein, can also be used to decrease  
15 or inhibit viral infection. Other exemplary agents are those identified using the methods described in the Examples below. These agents, such as antibodies, peptides, nucleic acids, organic or inorganic compounds, can be administered to a subject in a therapeutically effective amount. After the agent has produced an effect (a decreased level of viral infection is observed, or symptoms associated with viral infection decrease), for example after 24-48 hours, the subject can be monitored for  
20 diseases associated with viral infection.

The treatments disclosed herein can also be used prophylactically, for example to inhibit or prevent a viral infection. Such administration is indicated where the treatment is shown to have utility for treatment or prevention of the disorder. The prophylactic use is indicated in conditions known or suspected of progressing to disorders associated with a viral infection.

### Example 8

#### Recombinant Expression

With the disclosed host sequences involved in viral infection, native and variant sequences can be generated. Expression and purification by standard laboratory techniques of any variant, such  
30 as a polymorphism, mutant, fragment or fusion of a sequence involved in viral infection, such as a target sequence associated with SEQ ID NOS: 1-232, is enabled. One skilled in the art will understand that the sequences involved in viral infection, as well as variants thereof, can be produced recombinantly in any cell or organism of interest, and purified prior to use.

35 Methods for producing recombinant proteins are well known in the art. Therefore, the scope of this disclosure includes recombinant expression of any host protein or variant or fragment thereof involved in viral infection. For example, see U.S. Patent No: 5,342,764 to Johnson *et al.*; U.S. Patent No: 5,846,819 to Pausch *et al.*; U.S. Patent No: 5,876,969 to Fleer *et al.* and Sambrook *et al.* (*Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor, New York, 1989, Ch. 17, herein incorporated by reference).

Briefly, partial, full-length, or variant cDNA sequences that encode for a protein involved in viral infection, such as a target sequence associated with SEQ ID NOS: 1-232, can be ligated into an expression vector, such as a bacterial expression vector. Proteins or peptides can be produced by placing a promoter upstream of the cDNA sequence. Examples of promoters include, but are not limited to *lac*, *trp*, *tac*, *trc*, major operator and promoter regions of phage lambda, the control region of fd coat protein, the early and late promoters of SV40, promoters derived from polyoma, adenovirus, retrovirus, baculovirus and simian virus, the promoter for 3-phosphoglycerate kinase, the promoters of yeast acid phosphatase, the promoter of the yeast alpha-mating factors and combinations thereof.

Vectors suitable for the production of intact proteins include pKC30 (Shimatake and Rosenberg, 1981, *Nature* 292:128), pKK177-3 (Amann and Brosius, 1985, *Gene* 40:183) and pET-3 (Studier and Moffatt, 1986, *J. Mol. Biol.* 189:113). A DNA sequence can be transferred to other cloning vehicles, such as other plasmids, bacteriophages, cosmids, animal viruses and yeast artificial chromosomes (YACs) (Burke *et al.*, 1987, *Science* 236:806-12). These vectors can be introduced into a variety of hosts including somatic cells, and simple or complex organisms, such as bacteria, fungi (Timberlake and Marshall, 1989, *Science* 244:1313-7), invertebrates, plants (Gasser and Fraley, 1989, *Science* 244:1293), and mammals (Pursel *et al.*, 1989, *Science* 244:1281-8), that are rendered transgenic by the introduction of the heterologous cDNA.

For expression in mammalian cells, a cDNA sequence, such as a coding sequence of any target sequence associated with SEQ ID NOS: 1-227, 229, or 231, can be ligated to heterologous promoters, such as the simian virus SV40, promoter in the pSV2 vector (Mulligan and Berg, 1981, *Proc. Natl. Acad. Sci. USA* 78:2072-6), and introduced into cells, such as monkey COS-1 cells (Gluzman, 1981, *Cell* 23:175-82), to achieve transient or long-term expression. The stable integration of the chimeric gene construct may be maintained in mammalian cells by biochemical selection, such as neomycin (Southern and Berg, 1982, *J. Mol. Appl. Genet.* 1:327-41) and mycophenolic acid (Mulligan and Berg, 1981, *Proc. Natl. Acad. Sci. USA* 78:2072-6).

The transfer of DNA into eukaryotic, such as human or other mammalian cells is a conventional technique. The vectors are introduced into the recipient cells as pure DNA (transfection) by, for example, precipitation with calcium phosphate (Graham and vander Eb, 1973, *Virology* 52:466) strontium phosphate (Brash *et al.*, 1987, *Mol. Cell Biol.* 7:2013), electroporation (Neumann *et al.*, 1982, *EMBO J.* 1:841), lipofection (Felgner *et al.*, 1987, *Proc. Natl. Acad. Sci. USA* 84:7413), DEAE dextran (McCuthan *et al.*, 1968, *J. Natl. Cancer Inst.* 41:351), microinjection (Mueller *et al.*, 1978, *Cell* 15:579), protoplast fusion (Schafner, 1980, *Proc. Natl. Acad. Sci. USA* 77:2163-7), or pellet guns (Klein *et al.*, 1987, *Nature* 327:70). Alternatively, the cDNA can be introduced by infection with virus vectors, for example retroviruses (Bernstein *et al.*, 1985, *Gen. Engrg.* 7:235) such as adenoviruses (Ahmad *et al.*, *J. Virol.* 57:267, 1986) or Herpes (Spaete *et al.*, *Cell* 30:295, 1982).

### Pharmaceutical Compositions and Modes of Administration

Various delivery systems for administering the therapies disclosed herein are known, and include encapsulation in liposomes, microparticles, microcapsules, expression by recombinant cells, receptor-mediated endocytosis (Wu and Wu, *J. Biol. Chem.* 1987, 262:4429-32), and construction of therapeutic nucleic acids as part of a retroviral or other vector. Methods of introduction include, but are not limited to, topical, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, and oral routes. The compounds can be administered by any convenient route, for example by infusion or bolus injection, by absorption through epithelial or mucocutaneous linings (for example, oral mucosa, rectal, vaginal and intestinal mucosa, etc.) and can be administered together with other biologically active agents. Administration can be systemic or local. Pharmaceutical compositions can be delivered locally to the area in need of treatment, for example by topical application.

Pharmaceutical compositions are disclosed that include a therapeutically effective amount of an RNA, DNA, antisense molecule, ribozyme, RNAi molecule, siRNA molecule, specific-binding agent, or other therapeutic agent, alone or with a pharmaceutically acceptable carrier. Furthermore, the pharmaceutical compositions or methods of treatment can be administered in combination with (such as before, during, or following) other therapeutic treatments, such as other antiviral agents.

#### *Delivery systems*

The pharmaceutically acceptable carriers useful herein are conventional. *Remington's Pharmaceutical Sciences*, by Martin, Mack Publishing Co., Easton, PA, 15th Edition (1975), describes compositions and formulations suitable for pharmaceutical delivery of the therapeutic agents herein disclosed. In general, the nature of the carrier will depend on the mode of administration being employed. For instance, parenteral formulations usually include injectable fluids that include pharmaceutically and physiologically acceptable fluids such as water, physiological saline, balanced salt solutions, aqueous dextrose, sesame oil, glycerol, ethanol, combinations thereof, or the like, as a vehicle. The carrier and composition can be sterile, and the formulation suits the mode of administration. In addition to biologically-neutral carriers, pharmaceutical compositions to be administered can contain minor amounts of non-toxic auxiliary substances, such as wetting or emulsifying agents, preservatives, and pH buffering agents and the like, for example sodium acetate or sorbitan monolaurate.

The composition can be a liquid solution, suspension, emulsion, tablet, pill, capsule, sustained release formulation, or powder. For solid compositions (for example powder, pill, tablet, or capsule forms), conventional non-toxic solid carriers can include, for example, pharmaceutical grades of mannitol, lactose, starch, sodium saccharine, cellulose, magnesium carbonate, or magnesium stearate. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides.

Embodiments of the disclosure including medicaments can be prepared with conventional pharmaceutically acceptable carriers, adjuvants and counterions as would be known to those of skill in the art.

5 The amount of therapeutic agent effective in decreasing or inhibiting viral infection can depend on the nature of the virus and its associated disorder or condition, and can be determined by standard clinical techniques. In addition, *in vitro* assays can be employed to identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of the practitioner and each subject's circumstances. Effective doses can be extrapolated  
10 from dose-response curves derived from *in vitro* or animal model test systems.

The disclosure also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by  
15 the agency of manufacture, use or sale for human administration. Instructions for use of the composition can also be included.

#### *Administration of Nucleic Acids*

In an example in which a nucleic acid is employed to reduce viral infection, such as an  
20 antisense, RNAi molecule, or siRNA molecule, the nucleic acid can be delivered intracellularly (for example by expression from a nucleic acid vector or by receptor-mediated mechanisms), or by an appropriate nucleic acid expression vector which is administered so that it becomes intracellular, for example by use of a retroviral vector (see U.S. Patent No. 4,980,286), or by direct injection, or by use of microparticle bombardment (such as a gene gun; Biolistic, Dupont), or coating with lipids or cell-  
25 surface receptors or transfecting agents, or by administering it in linkage to a homeobox-like peptide which is known to enter the nucleus (for example Joliot *et al.*, *Proc. Natl. Acad. Sci. USA* 1991, 88:1864-8). The present disclosure includes all forms of nucleic acid delivery, including synthetic oligos, naked DNA, plasmid and viral, integrated into the genome or not.

30

#### **Example 10**

#### **in vitro Screening Assay for Agents that Decrease Viral Infection**

This example describes *in vitro* methods that can be used to screen test agents for their ability to interfere with or even inhibit viral infection of a host cell. As disclosed in the Examples above, the disclosed host proteins (such as those listed in Table 1 and the target protein sequences associated with SEQ ID NOS: 1-232, as well as variants, fragments, and fusions thereof) are involved in viral infection (such as infection by HIV, Ebola, and influenza A), and the host protein/viral protein interaction is a component in the ability of a virus to infect a cell. Therefore, screening assays can be used to identify and analyze agents that decrease or interfere with this interaction. For example, the following assays can be used to identify agents that interfere with the interaction of the disclosed host proteins (such as those listed in Table 1 and the target protein sequences associated with SEQ ID NOS: 1-232) with a viral protein sequence. However, the present disclosure is not limited to the particular methods disclosed herein.

Agents identified via the disclosed assays can be useful, for example, in decreasing or even inhibiting viral infection by more than an amount of infection in the absence of the agent, such as a decrease of at least about 10%, at least about 20%, at least about 50%, or even at least about 90%. This decrease in viral infection can serve to ameliorate symptoms associated with viral infection, such as fever. Assays for testing the effectiveness of the identified agents, are discussed below.

Exemplary test agents include, but are not limited to, any peptide or non-peptide composition in a purified or non-purified form, such as peptides made of D-and/or L-configuration amino acids (in, for example, the form of random peptide libraries; see Lam *et al.*, *Nature* 354:82-4, 1991), phosphopeptides (such as in the form of random or partially degenerate, directed phosphopeptide libraries; see, for example, Songyang *et al.*, *Cell* 72:767-78, 1993), antibodies, and small or large organic or inorganic molecules. A test agent can also include a complex mixture or "cocktail" of molecules.

The basic principle of the assay systems used to identify agents that interfere with the interaction between a host protein, such as those listed in Table 1 and the target protein sequences associated with SEQ ID NOS: 1-232, and its viral protein binding partner or partners, involves preparing a reaction mixture containing the host protein and a viral protein under conditions and for a time sufficient to allow the two proteins to interact and bind, thus forming a complex. In order to test an agent for inhibitory activity, the reaction is conducted in the presence and absence of the test agent. The test agent can be initially included in the reaction mixture, or added at a time subsequent to the addition of a host protein and a viral protein. Controls are incubated without the test agent or with a placebo. Exemplary controls include agents known not to bind to viral or host proteins. The formation of any complexes between the host protein and the viral protein is then detected. The formation of a complex in the control reaction, but not in the reaction mixture containing the test agent, indicates that the agent interferes with the interaction of the host protein and the viral protein, and is therefore possibly an agent that can be used to decrease viral infection.

The assay for agents that interfere with the interaction of host and viral proteins can be conducted in a heterogeneous or homogeneous format. Heterogeneous assays involve anchoring the host protein or the viral protein onto a solid phase and detecting complexes anchored on the solid



phase at the end of the reaction. In some examples, the method further involves quantitating the amount of complex formation or inhibition. Exemplary methods that can be used to detect the presence of complexes, when one of the proteins is labeled, include ELISA, spectrophotometry, flow cytometry, and microscopy. In homogeneous assays, the entire reaction is performed in a liquid phase. In either method, the order of addition of reactants can be varied to obtain different information about the agents being tested. For example, test agents that interfere with the interaction between the proteins, such as by competition, can be identified by conducting the reaction in the presence of the test agent, for example by adding the test agent to the reaction mixture prior to or simultaneously with the host protein and viral protein. On the other hand, test agents that disrupt preformed complexes, such as agents with higher binding constants that displace one of the proteins from the complex, can be tested by adding the test agent to the reaction mixture after complexes have been formed. The various formats are described briefly below.

Once identified, test agents found to inhibit or decrease the interaction between a host protein and a viral protein can be formulated in therapeutic products (or even prophylactic products) in pharmaceutically acceptable formulations, and used for specific treatment or prevention of a viral disease, such as HIV, Ebola, or influenza A.

#### *Heterogeneous assay system*

In a heterogeneous assay system, one binding partner, either the host protein (such as those listed in Table 1 and target protein sequences associated with SEQ ID NOS: 1-232) or the viral protein (such as an HIV, Ebola, or influenza A virus preparation) is anchored onto a solid surface (such as a microtiter plate), and its binding partner, which is not anchored, is labeled, either directly or indirectly. Exemplary labels include, but are not limited to, enzymes, fluorophores, ligands, and radioactive isotopes. The anchored protein can be immobilized by non-covalent or covalent attachments. Non-covalent attachment can be accomplished simply by coating the solid surface with a solution of the protein and drying. Alternatively, an immobilized antibody (such as a monoclonal antibody) specific for the protein can be used to anchor the protein to the solid surface. The surfaces can be prepared in advance and stored.

To conduct the assay, the binding partner of the immobilized species is added to the coated surface with or without the test agent. After the reaction is complete, unreacted components are removed (such as by washing) and any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the binding partner was pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the binding partner is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; for example by using a labeled antibody specific for the binding partner (the antibody, in turn, may be directly labeled or indirectly labeled with a labeled anti-Ig antibody). Depending upon the order of addition of reaction components, test compounds which inhibit complex formation or which disrupt preformed complexes can be detected.

Alternatively, the reaction can be conducted in a liquid phase in the presence or absence of the test agent, the reaction products separated from unreacted components, and complexes detected; for example by using an immobilized antibody specific for one binding partner to anchor any complexes formed in solution, and a labeled antibody specific for the other binding partner to detect anchored complexes. Again, depending upon the order of addition of reactants to the liquid phase, test agents which inhibit complex or which disrupt preformed complexes can be identified.

#### *Homogenous assays*

In an alternate example, a homogeneous assay can be used. In this method, a preformed complex of the host protein and the viral protein is prepared in which one of the proteins is labeled, but the signal generated by the label is quenched due to complex formation (for example, see U.S. Pat. No. 4,109,496 by Rubenstein which utilizes this approach for immunoassays). The addition of a test substance that competes with and displaces one of the binding partners from the preformed complex will result in the generation of a signal above background. In this way, test agents that disrupt host protein-viral protein interactions are identified.

#### *Immobilization of Proteins*

In a particular example, a host protein involved in viral infection (such as those listed in Table 1 and the target protein sequences associated with SEQ ID NOS: 1-232) can be prepared for immobilization using recombinant DNA techniques. For example, a coding region of a protein listed in Table 1, or any target sequence associated with SEQ ID NOS: 1-232, can be fused to a glutathione-S-transferase (GST) gene using the fusion vector pGEX-5X-1, in such a manner that its binding activity is maintained in the resulting fusion protein. The viral protein (such as an Ebola, HIV, or influenza A protein or viral preparation) can be purified and used to raise a monoclonal antibody, using methods routinely practiced in the art and described above. This antibody can be labeled with the radioactive isotope  $^{125}\text{I}$  using methods routinely practiced in the art.

In a heterogeneous assay, for example, the GST-host fusion protein can be anchored to glutathione-agarose beads. The viral protein preparation can then be added in the presence or absence of the test agent in a manner that allows interaction and binding to occur. At the end of the reaction period, unbound material can be washed away, and the labeled monoclonal antibody can be added to the system and allowed to bind to the complexed binding partners. The interaction between the host protein and the viral protein can be detected by measuring the amount of radioactivity that remains associated with the glutathione-agarose beads. A successful inhibition of the interaction by the test compound will result in a decrease in measured radioactivity.

Alternatively, the GST-host fusion protein and the viral protein can be mixed together in liquid in the absence of the solid glutathione agarose beads. The test agent can be added either during or after the binding partners are allowed to interact. This mixture can then be added to the glutathione-agarose beads and unbound material is washed away. Again, the extent of inhibition of

the binding partner interaction can be detected by adding the labeled antibody and measuring the radioactivity associated with the beads.

In another example, these same techniques can be employed using peptide fragments that correspond to the binding domains of the host protein and the viral protein, respectively, in place of one or both of the full length proteins. Any number of methods routinely practiced in the art can be used to identify and isolate the protein's binding site. These methods include, but are not limited to, mutagenesis of one of the genes encoding the proteins and screening for disruption of binding in a co-immunoprecipitation assay. Compensating mutations in a host gene can be selected. Sequence analysis of the genes encoding the respective proteins will reveal the mutations that correspond to the region of the protein involved in interactive binding. Alternatively, one protein can be anchored to a solid surface using methods described in above, and allowed to interact with and bind to its labeled binding partner, which has been treated with a proteolytic enzyme, such as trypsin. After washing, a short, labeled peptide comprising the binding domain may remain associated with the solid material, which can be isolated and identified by amino acid sequencing. Also, once the gene coding for the for the cellular or extracellular protein is obtained, short gene segments can be engineered to express peptide fragments of the protein, which can then be tested for binding activity and purified or synthesized.

For example, a host protein can be anchored to a solid material as described above by making a GST-host protein fusion protein and allowing it to bind to glutathione agarose beads. The viral protein can be labeled with a radioactive isotope, such as  $^{35}\text{S}$ , and cleaved with a proteolytic enzyme such as trypsin. Cleavage products can then be added to the anchored GST-host protein fusion protein and allowed to bind. After washing away unbound peptides, labeled bound material, representing the cellular or extracellular protein binding domain, can be eluted, purified, and analyzed for amino acid sequence. Peptides so identified can be produced synthetically or fused to appropriate facilitative proteins using recombinant DNA technology.

#### Example 11

##### Cell-Based Screening Assay for Agents that Decrease Viral Infection

This example describes methods using intact cells that can be used to screen test agents for their ability to interfere with or even inhibit viral infection of a host cell. For example, a yeast two-hybrid assay or the inverse two-hybrid assay method of Schreiber and coworkers (*Proc. Natl. Acad. Sci., USA* 94:13396, 1977) is used to screen for an agent that disrupts the association between a host protein (such as those listed in Table 1, proteins encoded by any target sequence associated with SEQ ID NOS: 1-227, 229, and 231, and any target sequence associated with SEQ ID NOS: 229, 230, and 232) and a viral protein (such as HIV, Ebola, or influenza A virus). Similar to Example 10, therapeutic agents identified by these approaches are tested for their ability to decrease or inhibit infection of a host cell, such as a human cell, by HIV, Ebola, or influenza A.

In one example, the yeast two-hybrid system is used to identify anti-viral agents. One version of this system has been described (Chien *et al.*, *Proc. Natl. Acad. Sci. USA*, 88:9578-82,

1991) and is commercially available from Clontech (Palo Alto, CA). Briefly, utilizing such a system, plasmids are constructed that encode two hybrid proteins: one includes the DNA-binding domain of a transcription activator protein fused to one test protein "X" and the other includes the activator protein's activation domain fused to another test protein "Y". Thus, either "X" or "Y" in this system  
5 can be a host protein (such as those listed in Table 1 and any target sequences associated with SEQ ID NOS: 1-232), while the other can be a test protein or peptide. The plasmids are transformed into a strain of *Saccharomyces cerevisiae* that contains a reporter gene (such as lacZ) whose regulatory region contains the activator's binding sites. Either hybrid protein alone cannot activate transcription of the reporter gene, the DNA-binding domain hybrid because it does not provide activation function  
10 and the activation domain hybrid because it cannot localize to the activator's binding sites. Interaction of the two proteins reconstitutes the functional activator protein and results in expression of the reporter gene, which is detected by an assay for the reporter gene product.

The two-hybrid system or related methodology can be used to screen activation domain libraries for proteins that interact with a host protein involved in viral infection. Total genomic or  
15 cDNA sequences are fused to the DNA encoding an activation domain. This library and a plasmid encoding a hybrid of the host protein involved in viral infection fused to the DNA-binding domain are cotransformed into a yeast reporter strain, and the resulting transformants are screened for those that express the reporter gene. These colonies are purified and the plasmids responsible for reporter gene expression are isolated. DNA sequencing is then used to identify the proteins encoded by the  
20 library plasmids.

For example, and not by way of limitation, a host gene encoding a protein involved in viral infection (such as those listed in Table 1 and target sequences associated with SEQ ID NOS: 1-232) can be cloned into a vector such that it is translationally fused to the DNA encoding the DNA-binding domain of the GAL4 protein. A cDNA library of the cell line from which proteins that interact with  
25 the host protein are to be detected can be made using methods routinely practiced in the art. In this particular system, the cDNA fragments can be inserted into a vector such that they are translationally fused to the activation domain of GAL4. This library can be co-transformed along with the host-GAL4 DNA binding domain fusion plasmid into a yeast strain which contains a lacZ gene driven by a promoter which contains GAL4 activation sequences. A cDNA encoded protein, fused to GAL4  
30 activation domain, that interacts with the host protein will reconstitute an active GAL4 protein and thereby drive expression of the lacZ gene. Colonies which express lacZ can be detected by their blue color in the presence of X-gal. The cDNA can then be extracted from strains derived from these and used to produce and isolate the host protein-interacting protein using techniques routinely practiced in  
35 the art.

#### Example 12

##### Rapid Screening Assays

Prior to performing any assays to detect interference with the association of a host protein involved in viral infection and a viral protein such as an HIV, Ebola, or influenza A protein, rapid

screening assays can be used to screen a large number of agents to determine if they bind to the host or viral protein. Rapid screening assays for detecting binding to HIV proteins have been disclosed, for example in U.S. Patent No. 5,230,998, which is incorporated by reference. In that assay, a host protein (such as those listed in Table 1 and target protein sequences associated with SEQ ID NOS: 1-232) or a viral protein, such as an HIV protein, is incubated with a first antibody capable of binding to the host or viral protein, and the agent to be screened. Excess unbound first antibody is washed and removed, and antibody bound to the host or viral protein is detected by adding a second labeled antibody which binds the first antibody. Excess unbound second antibody is then removed, and the amount of the label is quantitated. The effect of the binding effect is then determined in percentages by the formula:  $(\text{quantity of the label in the absence of the test agent}) - (\text{quantity of the label in the presence of the test agent} / \text{quantity of the label in the absence of the test agent}) \times 100$ .

Agents that are found to have a high binding affinity to the host or viral protein can then be used in other assays more specifically designed to test inhibition of the host protein/viral protein interaction, or inhibition of viral replication.

### Example 13

#### Assays for Measuring Inhibition of Viral Infection

Any of the test agents identified in the foregoing assay systems can be tested for their ability to decrease or inhibit infection by a pathogen or virus such as HIV, Ebola, or influenza A.

#### *Cell-based assays*

Exemplary methods are provided in Example 3 above. Briefly, cells (20,000 to 250,000) are infected with the desired pathogen, such as HIV, Ebola, or influenza A, and the incubation continued for 3-7 days. The test agent can be applied to the cells before, during, or after infection with the virus. The amount of virus and agent administered can be determined by skilled practitioners. In some examples, several different doses of the potential therapeutic agent can be administered, to identify optimal dose ranges. Following transfection, assays are conducted to determine the resistance of the cells to infection by various agents.

For example, the presence of a viral antigen can be determined by using antibody specific for the viral protein then detecting the antibody. In one example, the antibody that specifically binds to the viral protein is labeled, for example with a detectable marker such as a fluorephore. In another example, the antibody is detected by using a secondary antibody-containing a label. The presence of bound antibody is then detected, for example using microscopy, flow cytometry, and ELISA.

Alternatively or in addition, the ability of the cells to survive viral infection is determined, for example by performing a cell viability assay, such as trypan blue exclusion.

#### *Animal model assays*

The ability of an agent, such as those identified using the methods provide above, to prevent or decrease infection by a virus, such as HIV, Ebola, or influenza A, can be assessed in animal

models. Several animal models for viral infection are known in the art. For example, mouse HIV models are disclosed in Sutton *et al.* (*Res. Initiat. Treat. Action*, 8:22-4, 2003) and Pincus *et al.* (*AIDS Res. Hum. Retroviruses* 19:901-8, 2003); guinea pig models for Ebola infection are disclosed in Parren *et al.* (*J. Virol.* 76:6408-12, 2002) and Xu *et al.* (*Nat. Med.* 4:37-42, 1998); and cynomolgus monkey (*Macaca fascicularis*) models for influenza infection are disclosed in Kuiken *et al.* (*Vet. Pathol.* 40:304-10, 2003). Such animal models can also be used to test agents for an ability to ameliorate symptoms associated with viral infection. In addition, such animal models can be used to determine the LD50 and the ED50 in animal subjects, and such data can be used to determine the *in vivo* efficacy of potential agents.

5. Animals of any species, including, but not limited to, mice, rats, rabbits, guinea pigs, pigs, micro-pigs, goats, and non-human primates, such as baboons, monkeys, and chimpanzees, can be used to generate an animal model of viral infection if needed.

- 10 The appropriate animal is inoculated with the desired virus, in the presence or absence of the test agents identified in the examples above. The amount of virus and agent administered can be determined by skilled practitioners. In some examples, several different doses of the potential therapeutic agent can be administered to different test subjects, to identify optimal dose ranges. The therapeutic agent can be administered before, during, or after infection with the virus. Subsequent to the treatment, animals are observed for the development of the appropriate viral infection and symptoms associated therewith. A decrease in the development of the appropriate viral infection, or symptoms associated therewith, in the presence of the test agent provides evidence that the test agent is a therapeutic agent that can be used to decrease or even inhibit viral infection in a subject.

- 15 Having illustrated and described the principles of the invention by several examples, it should be apparent that those embodiments can be modified in arrangement and detail without departing from the principles of the invention. Thus, the invention includes all such embodiments and variations thereof, and their equivalents.

## We claim:

1. A method of decreasing infection of a host cell by a virus, comprising interfering with an activity or expression of one or more host proteins or interfering with an activity of one or more host nucleic acids, wherein the host protein or host nucleic acid is a T-cell receptor V beta chain; T-cell receptor V-D-J beta 2.1 chain;  $\beta$ -chimerin; malic enzyme 1; hypothetical protein XP\_174419; sequence from chromosome 4q31.3-32; alpha satellite DNA; LOC253788; LOC219938; coagulation factor III (F3); LOC91759; similar to KOX4 (LOC131880); LOC166140; LOC222474; similar to Rho guanine nucleotide exchange factor 4, isoform a; APC-stimulated guanine nucleotide exchange factor (LOC221178); T-cell receptor beta; ribosomal protein L7A-like 4; v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian) (SRC); KIAA0564; alpha satellite DNA; M96 protein; hypothetical protein similar to G proteins (LOC57826); LOC161005; osteoblast specific factor 2; Canis familiaris T-cell leukemia translocation-associated protein; aminomethyltransferase; dystroglycan; bassoon; LIM domain containing preferred translocation partner in lipoma; sequence between LOC253121 and hyaluronan synthase 2; testin 2, testin 3; protein tyrosine phosphatase, non-receptor type 1; sequence between LOC149360 and LOC253961; sequence between KIAA1560 and tectorin beta; cadherin related 23; myeloid/lymphoma or mixed lineage leukemia, translocated to 10; exportin 5; DNA polymerase eta (POLH); heterogenous nuclear riboprotein C (C1/C2); alpha-endosulfine pseudogene; LOC128741; LOC222888; LOC138421; zinc finger protein 297B; sideroflexin 5; importin 9 (FLJ10402); T-cell receptor beta; similar to murine putative transcription factor ZNF131 (LOC135952); KIAA1259; MURR1; CCT4; FLJ40773; similar to ribosomal protein L24-like (LOC149360); polybromo 1; DNA damage inducible transcript 3; KIAA1887; PDZ; LIM domain 1 (elfin); LOC284803; PRO0097; FLJ31958; small inducible cytokine E, member 1 (endothelial monocyte-activating); E3 ubiquitin ligase (SMURF2); MGC40489; Rab9; PRO1617; retinoblastoma binding protein 1; region of chromosome 2q12; elongation factor for selenoprotein translation; Transcription factor SMIF (HSA275986); KIAA1026; trinucleotide repeat containing 5 (TNRC5); homogentisate 1,2-dioxygenase (HGD); region of chromosome Xq23-24; region of chromosome 4p15.3; similar to LWarnide neuropeptide precursor protein [Hydractinia echinata] (LOC129883); region of chromosome 2q21; region of chromosome Xp11.4, including UPS9X; LOC221829; U3 small nuclear RNA; integrin, beta 1 (ITGB1); acrosomal vesicle protein 1 (ACRV1) and CHK1 checkpoint homolog (CHEK1); prospero-related homeobox 1 (PROX1); FLJ20627 and FLJ12910; PIN2-interacting protein (PINX1) and SRY (sex-determining region Y)-box 7 (SOX7); LOC131920; region of chromosome 13q14; neurotrophic tyrosine kinase, receptor, type 3 (NTRK3); TERA protein and FLJ13224; LOC284260; POM (POM121 homolog) and ZP3 fusion (POMZP3); DEAD/H box polypeptide 8 (DDX8) and similar to ribosomal protein L29 (cell surface heparin binding protein HIP) (LOC284064); LOC345307 and UDP-N-acetyl-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNT7); Mus musculus 5S rRNA pseudogene (Rn5s-ps1); ribosomal protein L27a pseudogene (RPL27AP) and v-myb myeloblastosis viral oncogene homolog-like 2 (MYBL2); Down's syndrome-cell adhesion molecule like 1 (DSCAML1); LOC148529; Huntingtin-associated protein interacting protein (HAPIP); LOC158525

and similar to RIKEN cDNA 1210001E11 (LOC347366); hypothetical protein FLJ12910; LOC350411; allograft inflammatory factor 1 (AIF1) and HLA-B associated transcript 2 (BAT2); C10orf7; LOC346658 and LOC340349; region of chromosome 12q21; LOC339248 and FLJ22659; SR rich protein DKFZp564B0769 and hypothetical protein MGC14793; FLJ10439; cytochrome P450, family 11, subfamily A, polypeptide 1 (CYP11A1) and sema domain, immunoglobulin domain (Ig) and GPI membrane anchor, (semaphoring) 7A; ribosomal protein S16 (RPS16); hypothetical protein DKFZp434H0115 and ATP citrate lyase (ACLY); calnexin (CANX); protein tyrosine phosphatase, receptor type, K (PTPRK); cyclin M2 (CNNM2); or AXL receptor tyrosine kinase (AXL), and wherein interfering with the activity or expression of the one or more host proteins decreases infection of the host cell by the virus.

2. The method of claim 1, wherein the one or more host proteins is encoded by one or more host nucleic acids comprising at least 90% identity to any target nucleic acid sequence associated with SEQ ID NOS: 1-227, 229 or 231.

3. The method of claim 2, wherein the one or more host nucleic acids comprises any target nucleic acid sequence associated with SEQ ID NOS: 1-227, 229 or 231.

4. The method of claim 1, wherein the method comprises interfering with an activity or expression of more than one of the host proteins.

5. The method of claim 1, wherein the method comprises interfering with an activity or expression of at least three of the host proteins.

6. The method of claim 1 wherein the virus is HIV-1 or HIV-2, and the host protein or host nucleic acid is a T-cell receptor V beta chain; T-cell receptor V-D-J beta 2.1 chain;  $\beta$ -chimerin; malic enzyme 1; hypothetical protein XP\_174419; sequence from chromosome 4q31.3-32; alpha satellite DNA; LOC253788; LOC219938; coagulation factor III; LOC91759; similar to KOX4 (LOC131880); LOC166140; LOC222474; similar to Rho guanine nucleotide exchange factor 4, isoform a; APC-stimulated guanine nucleotide exchange factor (LOC221178); T-cell receptor beta; ribosomal protein L7A-like 4 (RPL7AL4); v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian) (SRC); KIAA0564; alpha satellite DNA; M96 protein; hypothetical protein similar to G proteins; RAP-2A (LOC57826); LOC161005; Rab9, or osteoblast specific factor 2.

7. The method of claim 6, wherein the method comprises interfering with an activity or expression of more than one of the host proteins.

8. The method of claim 6, wherein the method comprises interfering with expression of one or more of the host nucleic acids.



9. The method of claim 1 wherein the virus is influenza A, and the host protein is a *Canis familiaris* T-cell leukemia translocation-associated protein, aminomethyltransferase; dystroglycan; bassoon; LIM domain containing preferred translocation partner in lipoma; sequence between LOC253121 and hyaluronan synthase 2; testin 2; testin 3; PTPN1 gene for protein tyrosine phosphatase, non-receptor type 1; sequence between LOC149360 and LOC253961; sequence between KIAA1560 and tectorin beta; cadherin related 23; malic enzyme 1; hypothetical protein XP\_174419; sequence from chromosome 4q31.3-32; Rab9, or a myeloid/lymphoma or mixed lineage leukemia, translocated to 10.

10. The method of claim 9, wherein the method comprises interfering with an activity or expression of more than one of the host proteins.

11. The method of claim 9, wherein the method comprises interfering with expression of one or more of the host nucleic acids.

12. The method of claim 1 wherein the virus is Ebola, and the host protein is a exportin 5; DNA polymerase eta (POLH); heterogenous nuclear riboprotein C; alpha-endosulfine pseudogene; LOC128741; LOC222888; LOC138421; zinc finger protein 297B; sideroflexin 5; importin 9 (FLJ10402); T-cell receptor beta; similar to murine putative transcription factor ZNF131 (LOC135952); KIAA1259; MURR1; CCT4; FLJ40773; ribosomal protein L24-like (LOC149360); testin 2; testin 3; polybromo 1; DNA damage inducible transcript 3; KIAA1887; PDZ; LIM domain 1 (elfin); LOC284803; PRO0097; FLJ31958; small inducible cytokine E, member 1 (endothelial monocyte-activating); E3 ubiquitin ligase; MGC40489; Rab9; PRO1617; retinoblastoma binding protein 1; region of chromosome 2q12; elongation factor for selenoprotein translation; Transcription factor SMIF (HSA275986); KIAA1026; trinucleotide repeat containing 5 (TNRC5); homogentisate 1,2-dioxygenase (HGD); region of chromosome Xq23-24; region of chromosome 4p15.3; similar to LWamide neuropeptide precursor protein [*Hydractinia echinata*] (LOC129883); region of chromosome 2q21; region of chromosome Xp11.4, including UPS9X; LOC221829; U3 small nuclear RNA; integrin, beta 1 (ITGB1); acrosomal vesicle protein 1 (ACRV1) and CHK1 checkpoint homolog (CHEK1); prospero-related homeobox 1 (PROX1); FLJ20627 and FLJ12910; PIN2-interacting protein (PINX1) and SRY (sex-determining region Y)-box 7 (SOX7); LOC131920; region of chromosome 13q14; neurotrophic tyrosine kinase, receptor, type 3 (NTRK3); TERA protein and FLJ13224; LOC284260; POM (POM121 homolog) and ZP3 fusion (POMZP3); DEAD/H box polypeptide 8 (DDX8) and similar to ribosomal protein L29 (cell surface heparin binding protein HIP) (LOC284064); LOC345307 and UDP-N-acetyl-D-galactosamine:polypeptide N-acetyl-galactosaminyltransferase 7 (GALNT7); *Mus musculus* 5S rRNA pseudogene (Rn5s-ps1); ribosomal protein L27a pseudogene (RPL27AP) and v-myb myeloblastosis viral oncogene homolog-like 2 (MYBL2); Down's syndrome cell adhesion molecule like 1 (DSCAML1); LOC148529;

Huntingtin-associated protein interacting protein (HAIP); LOC158525 and similar to RIKEN cDNA 1210001E11 (LOC347366); hypothetical protein FLJ12910; LOC350411; allograft inflammatory factor 1 (AIF1) and HLA-B associated transcript 2 (BAT2); C10orf7; LOC346658 and LOC340349; region of chromosome 12q21; LOC339248 and FLJ22659; SR rich protein DKFZp564B0769 and  
5 hypothetical protein MGC14793; FLJ10439; cytochrome P450, family 11, subfamily A, polypeptide 1 (CYP11A1) and sema domain, immunoglobulin domain (Ig) and GPI membrane anchor, (semaphoring) 7A; ribosomal protein S16 (RPS16); hypothetical protein DKFZp434H0115 and ATP citrate lyase (ACLY); calnexin (CANX); protein tyrosine phosphatase, receptor type, K (PTPRK); cyclin M2 (CNNM2); or AXL receptor tyrosine kinase.

10

13. The method of claim 12, wherein the method comprises interfering with an activity or expression of more than one of the host proteins.

15

14. The method of claim 12, wherein the method comprises interfering with expression of one or more of the host nucleic acids.

20

15. The method of claim 6, wherein the one or more host proteins are encoded by one or more nucleic acid sequences comprising at least 90% identity to any target nucleic acid sequence associated with SEQ ID NOS: 1-35.

25

16. The method of claim 6, wherein one or more host proteins is encoded by one or more nucleic acid sequences comprising any target nucleic acid sequence associated with SEQ ID NOS: 1-35.

30

17. The method of claim 9, wherein the one or more host proteins are encoded by one or more nucleic acid sequences comprising at least 90% identity to any of SEQ ID NOS: 36-63 or a coding sequence of any of SEQ ID NOS: 36-63.

18. The method of claim 9, wherein the one or more host proteins are encoded by one or more nucleic acid sequences comprising any target nucleic acid sequence associated with SEQ ID NOS: 36-63.

35

19. The method of claim 12, wherein the one or more host proteins are encoded by one or more nucleic acid sequences comprising at least 90% identity to any target nucleic acid sequence associated with SEQ ID NOS: 64-227, 229, and 231.

20. The method of claim 12, wherein one or more host proteins are encoded by one or more nucleic acid sequences comprising any target nucleic acid sequence associated with SEQ ID NOS: 64-227, 229, and 231.

21. The method of claim 1, wherein interfering with the activity of the one or more host proteins comprises decreasing an interaction of a viral protein and the one or more host proteins by disrupting or decreasing expression of the one or more host proteins.

5

22. The method of claim 21, wherein the viral protein comprises a virus and decreasing the interaction of the viral protein and the one or more host proteins decreases or inhibits infection of a host cell by the virus.

10

23. The method of claim 21, wherein disrupting or decreasing expression of the host protein comprises disrupting or decreasing transcription of an mRNA encoding the host protein.

15

24. The method of claim 23, wherein disrupting or decreasing transcription of the mRNA comprises inserting a transposon or insertional vector into a coding region of the nucleic acid encoding the host protein.

20

25. The method of claim 23, wherein disrupting or decreasing the transcription of the mRNA comprises contacting the mRNA with an antisense RNA, RNAi, ribozyme, or siRNA that recognizes the mRNA.

25

26. The method of claim 1 wherein interfering with the activity of the host protein comprises decreasing an interaction of a viral protein and the host protein by contacting the cell with an agent that decreases or inhibits the activity or expression of the host protein or that disrupts expression of the host protein.

27. The method of claim 26, wherein the host cell is present in a host subject and wherein contacting the cell with the agent comprises administering the agent to the subject.

30

28. The method of claim 1, wherein the host cell is a mammalian host cell.

29. A method of decreasing HIV, Ebola, or influenza A infection of a host cell, comprising, decreasing an interaction between a viral nucleic acid and a host nucleic acid by decreasing the integration of the viral nucleic acid into the host nucleic acid, wherein the host nucleic acid comprises at least 90% identity to any target sequence associated with SEQ ID NOS: 1-227, 229, and 231.

35

30. The method of claim 29, wherein the viral nucleic acid comprises a viral genome and the host nucleic acid comprises a host genome.

31. A method of treating an HIV, Ebola, or influenza A viral infection in a host subject, comprising administering to a subject having a viral infection an effective amount of an agent that interferes with the interaction of a virus and host protein, wherein the host protein is encoded by a nucleic acid comprising at least 90% identity to any target sequence associated with SEQ ID NOS: 1-227, 229, and 231.

32. The method of claim 31, wherein the agent disrupts expression of the nucleic acid encoding the host protein.

33. The method of claim 32, wherein the agent is an antisense, ribozyme, or siRNA molecule that recognizes the nucleic acid sequence comprising at least 90% identity to any target sequence associated with SEQ ID NOS: 1-227, 229, and 231.

34. The method of claim 31, wherein the effective amount induces a prophylactic effect in the host, which inhibits infection of the host by a virus.

35. The method of claim 31, wherein the host was previously infected by a virus and the effective amount induces a therapeutic effect in the host.

36. A method of determining resistance or susceptibility to viral infection in a subject, comprising comparing a first nucleic acid sequence of a subject to a second nucleic acid sequence comprising any target sequence associated with SEQ ID NOS: 1-227, 229, and 231, wherein a higher similarity between the first and second nucleic acid sequence indicates the subject is more susceptible to viral infection, and wherein a lesser similarity between the first and second nucleic acid sequence indicates the subject is more resistant to viral infection.

37. The method of claim 36, wherein the first nucleic acid sequence is obtained from a biological sample of the subject.

38. The method of claim 37, wherein the first nucleic acid sequence comprises a plurality of nucleic acid sequences, wherein each nucleic acid sequence is obtained from a different subject.

39. The method according to claim 36, further comprising determining a polymorphic variation within a population.

40. A method of decreasing HIV, Ebola, or influenza A infection of a host cell, comprising: contacting the host cell with an anti-protein binding agent that selectively or specifically binds to a host protein encoded by any target sequence associated with SEQ ID NOS: 1-227, 229, and 231 or a protein sequence shown in any of SEQ ID NOS: 228, 230, or 232, wherein the anti-protein

binding agent inhibits an interaction between the host protein and the HIV, Ebola, or influenza A virus.

5 41. The method of claim 40, wherein the host cell is present in a subject, and contacting the host cell with the anti-protein binding agent comprises administering the anti-protein binding agent to the subject.

10 42. The method of claim 40, wherein the anti-protein binding agent is an antibody or chemical compound.

43. A method of identifying a compound that decreases binding of a viral protein to a host protein and decreases viral infection, comprising:

15 contacting the host protein with the viral protein and a test compound, wherein the host protein is a protein in Table 1, and the viral protein is an HIV, Ebola, or influenza A protein; and determining whether binding of the viral protein to the host protein is decreased in the presence of the test compound, the decrease in binding being an indication that the test compound decreases the binding of viral protein to the target protein, and decreases viral infection.

20 44. The method of claim 43, wherein the viral protein comprises a virus.

45. The method of claim 43, wherein the viral protein is a viral envelope protein.

25 46. The method of claim 43, wherein the viral protein is an HIV protein and the host protein is a protein encoded by a target sequence associated with SEQ ID NOS: 1-35.

47. The method of 43, wherein the viral protein is an influenza A protein and the host protein is a protein encoded by a target sequence associated with SEQ ID NOS: 36-63.

30 48. The method of claim 43, wherein the viral protein is an Ebola protein and the host protein is a protein encoded by a target sequence associated with SEQ ID NOS: 64-227, 229, and 231.

35 49. The method of claim 43, wherein the method comprises expressing the host protein in a cell, and contacting the host protein with the viral protein and a test compound comprises exposing the cell to the viral protein and the test compound.

50. The method of claim 43, wherein the host protein or the viral protein comprises a label, and determining whether binding is decreased comprises detecting an amount of label present.

51. A method of decreasing infection of a host cell by a pathogen, comprising interfering with an activity or expression of a Rab9 in the host cell, wherein interfering with Rab9 activity or expression decreases infection of the host cell by the pathogen.

52. The method of claim 51, wherein the pathogen hijacks a lipid raft.

53. The method of claim 51, wherein the pathogen is a *Campylobacter jejuni*, *Vibrio cholerae*, SV40, *Legionella pneumophila*, *Aeromonas hydrophilia*, Echovirus 1, Echovirus 11, *Brucella* spp, *Clostridium* spp., Avian sarcoma and leukosis virus, FimH, Dr *Escherichia coli*, *Streptococcus pyogenes*, Semiliki forest virus, *Salmonella typhimurium*, *Bacillus anthracis*, Ecotropic mouse leukaemia virus, *Shigella flexneri*, *Bacillus thuringiensis*, HTLV-1, *Chlamydia* spp., *Helicobacter pylori*, HIV-1, *Mycobacterium* spp., *Listeria monocytogenes*, Ebola, Marburg, Measles, Herpes Simplex virus, influenza virus, or Epstein-Barr virus.

54. The method of claim 51, wherein the Rab9 host protein is encoded by a host nucleic acid comprising at least 90% identity to a target sequence associated with any of SEQ ID NOS: 118-119.

55. The method of claim 54, wherein the host nucleic acid comprises a target sequence associated with any of SEQ ID NOS: 118-119.

56. The method of claim 51, wherein interfering with expression of Rab9 comprises disrupting or decreasing transcription of an mRNA encoding the Rab9 protein.

57. The method of claim 56 wherein disrupting or decreasing the transcription of the mRNA comprises contacting the mRNA with an antisense RNA, ribozyme, or siRNA that recognizes the mRNA.

58. The method of claim 57, wherein the siRNA sequence comprises any of SEQ ID NOS: 232-235.

59. The method of claim 57, wherein the host cell is present in a subject, and contacting the mRNA with an antisense RNA, ribozyme, or siRNA that recognizes the mRNA comprises administering the antisense RNA, ribozyme, or siRNA to the subject.

60. A cell comprising a functional deletion of one or more target sequences associated with any of SEQ ID NOS: 1-35, wherein the cell has a decreased susceptibility to HIV infection.

61. A cell comprising a functional deletion of one or more target sequences associated with any of SEQ ID NOS: 36-63, wherein the cell has a decreased susceptibility to influenza infection.

5 62. A cell comprising a functional deletion of one or more target sequences associated with any of SEQ ID NOS: 64-232, wherein the cell has a decreased susceptibility to Ebola infection.

63. A cell comprising a functional deletion of a Rab9 gene, wherein the cell has a decreased susceptibility to infection by a pathogen that uses lipid rafts.

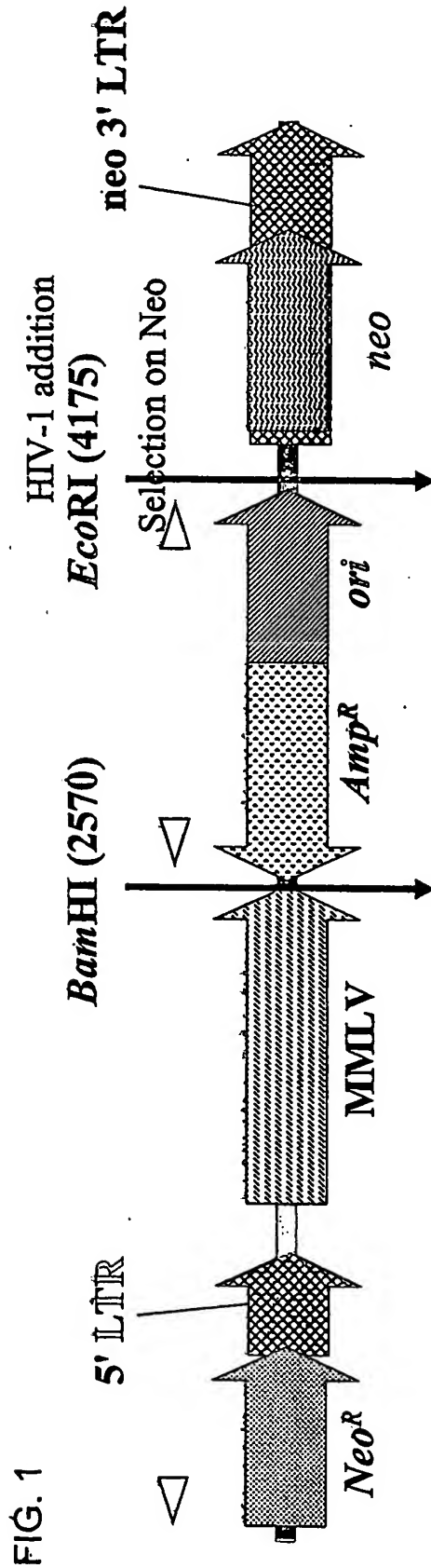
10 64. A non-human transgenic mammal comprising a functional deletion of one or more target sequences associated with any of SEQ ID NOS: 1-35, wherein the mammal has decreased susceptibility to infection by HIV.

15 65. A non-human transgenic mammal comprising a functional deletion of one or more target sequences associated with any of SEQ ID NOS: 36-63, wherein the mammal has decreased susceptibility to infection by influenza.

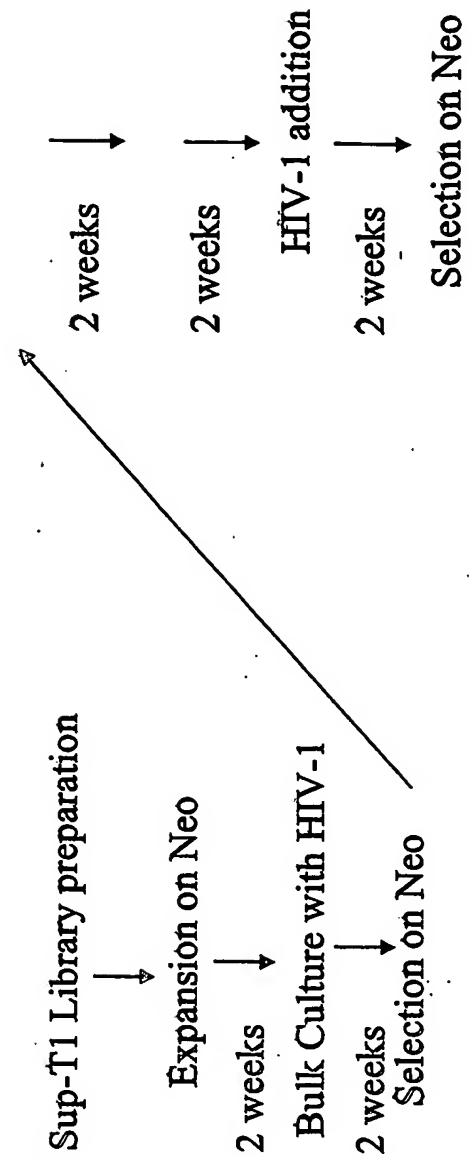
20 66. A non-human transgenic mammal comprising a functional deletion of one or more target sequences associated with any of SEQ ID NOS: 64-232, wherein the mammal has decreased susceptibility to infection by Ebola.

67. A non-human transgenic mammal comprising a functional deletion of a Rab9 gene, wherein the mammal has decreased susceptibility to infection by a pathogen that uses a lipid raft.

25 68. The method of claim 1, wherein interfering with an activity of the host nucleic acid comprising administering one or more of SEQ ID NOS: 246- 845 to the host cell.

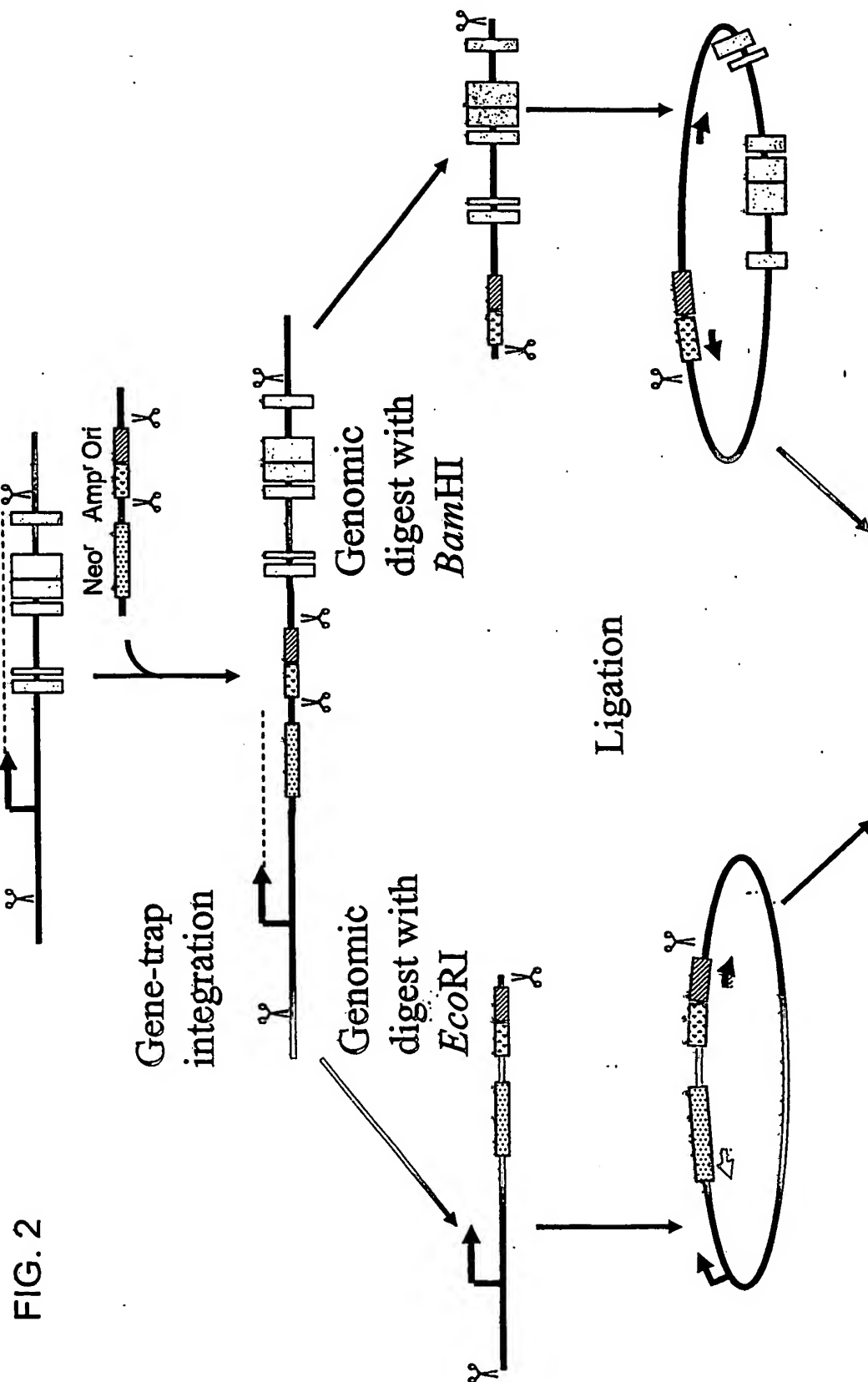


**FIG. 4**





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Recover clones by transformation into bacteria and sequence

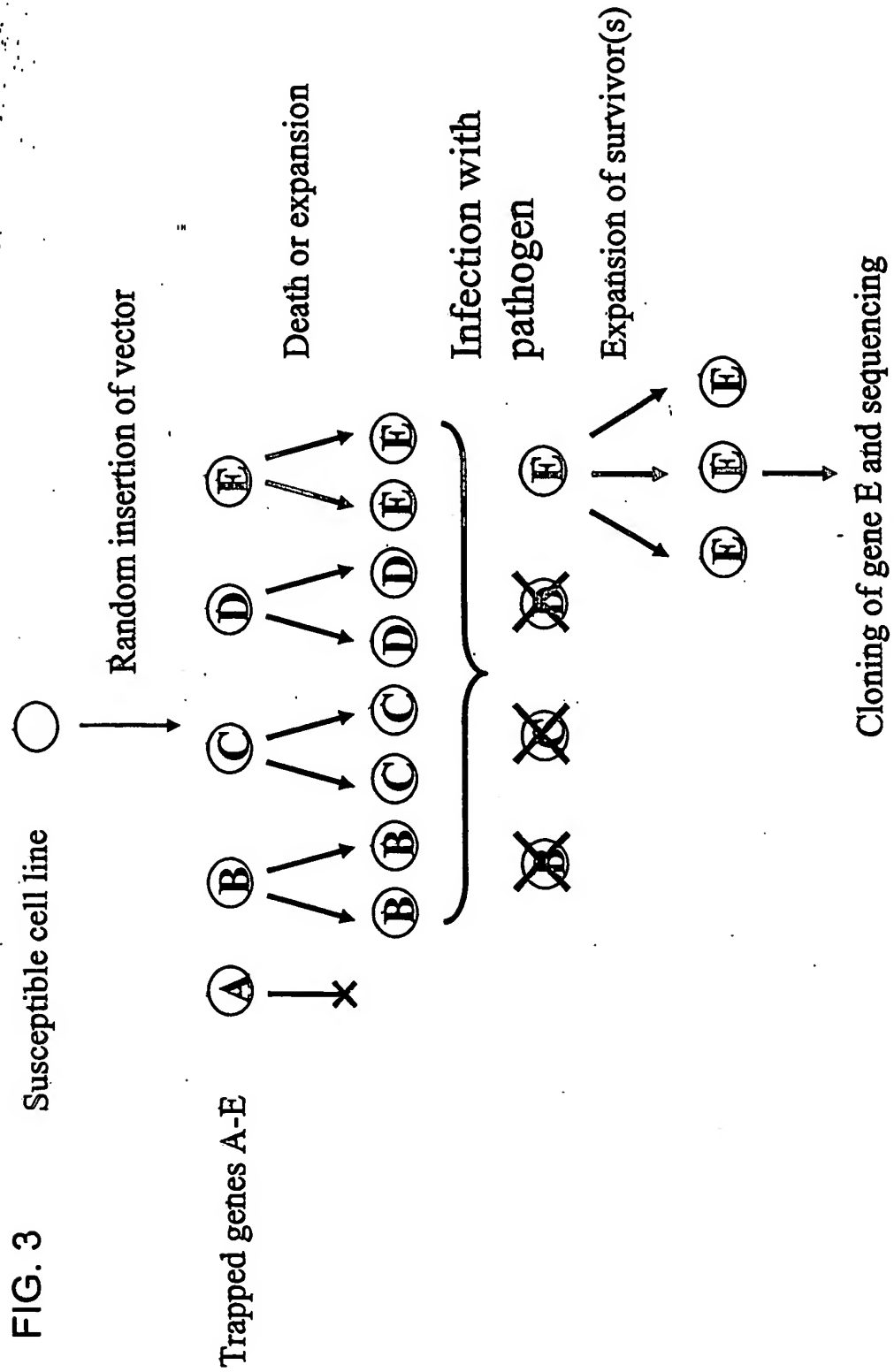
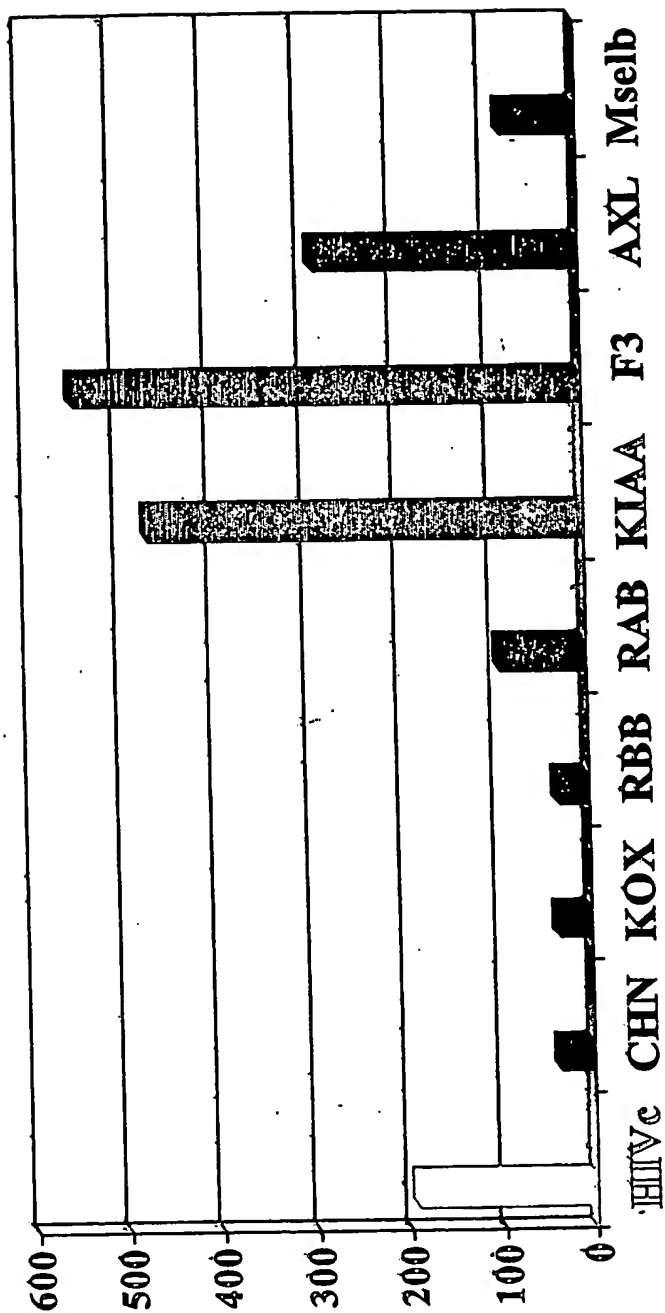
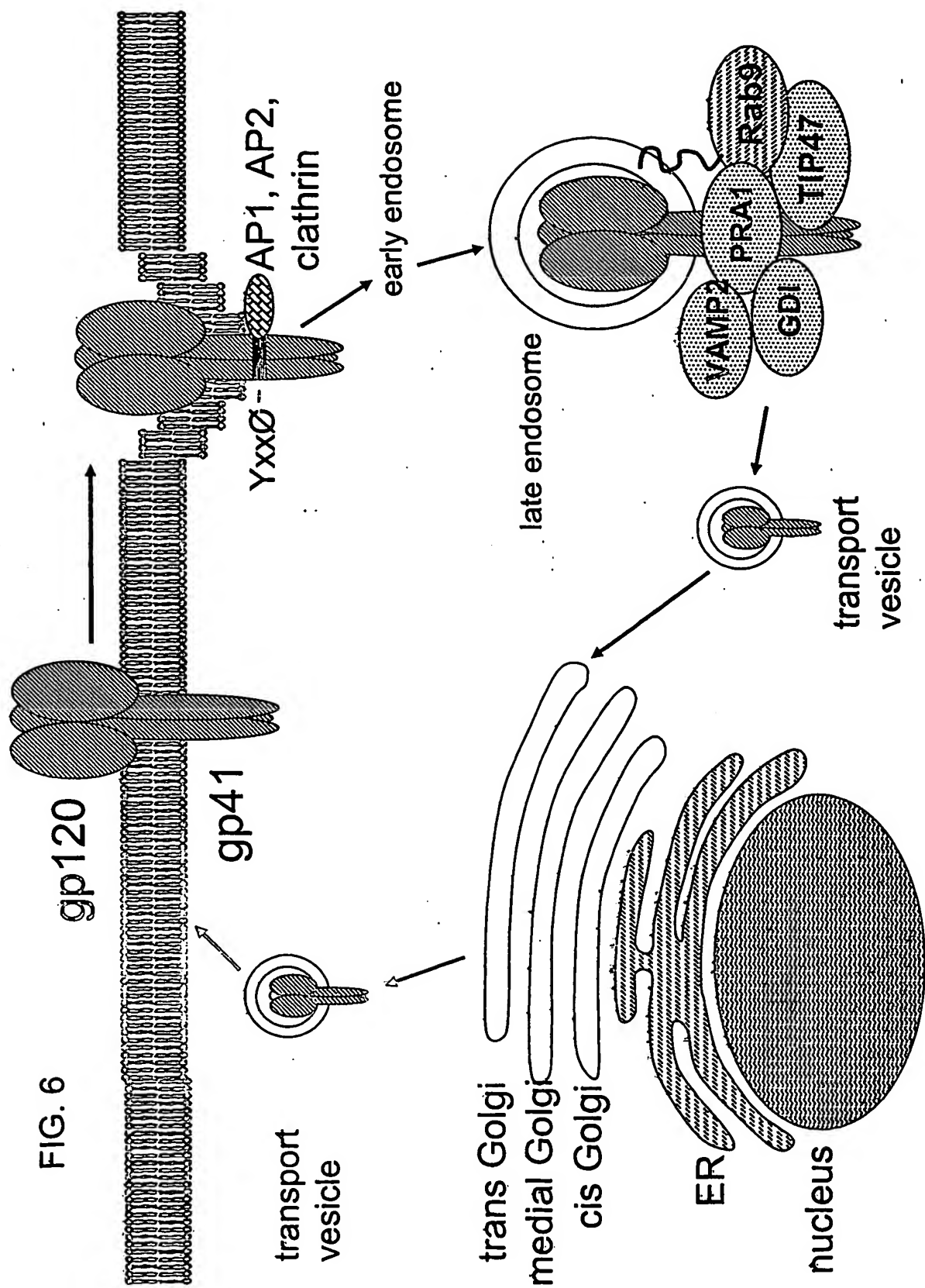


FIG. 5



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STATEMENT ACCOMPANYING SEQUENCE LISTING

The sequence listing does not include matter that goes beyond the disclosure in the international application.

The printout of the attached Sequence Listing is identical to the computer readable sequence listing on the enclosed computer disk.

## SEQUENCE LISTING

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 ctcggggcgc cagtctccg attgactgag tcgcccgggt acccggtat ccaataaacc 420  
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 accaggcct ccagttctc attcagtatt ataattggaga agagagagca aaaggaaaca 600  
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 gagagagggt gagcagccca ncctgnncga ccccanancc tgttnttagg ggagtggnc 840  
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<210> 4  
 <211> 900  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(900)  
 <223> n is a, g, c, or t

<400> 4



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 gaaaagcata cccacacagtg tcagtggagg caacatgggg tcttgattt cctcttcacc 180  
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 gcagaggcct agagagtagc ccaaaaactc atctgcacc agcaggactg aggtttccta 420  
 cccccaccaa tggaagccaa gtgaggaacc taagccttca cctctcactc agcaggaacc 480  
 agacaacacc ccctaacaca cacacacaca cacacacaca cacacccttc tgttagtgtg 540  
 gtatcaagga ggcttgataa aatagaagat ttaaatagga tccattgccc ttatctcaaa 600  
 ctcttattat gaaatcactc ccttgagaga gaaaaaagcc tttttctctt ggattgtccc 660  
 agcagctccc gaccatcccc actcccaac cttatgtggc cccagcaatg agcctagtag 720  
 taggaaaatc tctatggata ctggtgctga tgggaagatt ctctctctca ngaagtgtg 780  
 gtgactgggg ctctgggatg ctcacgggaa tncatttcc cccacaagaa nttattttat 840  
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<210> 5  
 <211> 869  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(869)  
 <223> n is a, g, c, or t

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 ctactccatg ctaagttcag cgagaacttg ggtacccta gacattcttc cagagatgct 180  
 tttcttgtaa ctcttttcaa taagtaagca tgctttgctc tgcactgggt gtcacctgtg 240  
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 atgcttaggt cagccctgag gtttgaacca gtcaacaagt ccaggttgggt gtggagtccc 360  
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 ctggaggggc cttgtgacca ttctgggtt actcctcttg ttccagcatc ccatgtggcc 480  
 aatgggcccc ttccatttcc aatggatatc caattcttac agtaagttat attattgccc 540  
 tacatcgaac tcatcttttc tcagtgttac ctgaggaaga atggagagga tgcccagaat 600

tggccagaa gaatccactt cgattctaga gaaaaaggca ggtagaggca gaagagattc 660  
 acttcccagt gcatgcgtgc tgaatgttgg ggggtgttgg tgagagagac aaggaaatgg 720  
 ctgtaaaact tgggaagagg aacctgccct ggggtcaagta ggggtgttggg aggaccagat 780  
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<210> 6  
 <211> 850  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(850)  
 <223> n is a, g, c, or t

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 tgcaaggcat ggaaaaatac ataactgaga atagaaaagt tcagatcgag gtcaggaaca 180  
 gatggaacag ggtcgaccgg tcgaccggtc gaccctagag aaccatcaga tgtttccagg 240  
 gtgcccgaag gacctgaaat gacctgtgc cttatttgaa ctaaccaatc agttcgcttc 300  
 tcgcttctgt tcgcgcgctt ctgctccccg agctcaataa aagagccac aaccctcac 360  
 tcggggcgcc agtcctccga ttgactgagt cgcccggtta cccgtgtatc caataaacc 420  
 tcttgagtt gcatccgact tgtggtctcg ctgttcttg ggagggtctc ctctgagtga 480  
 ttgactacc gtcagcgggg gtctttcact ctctgtgtac tggtagcaac agagcctgga 540  
 ccagggcctc cagttcctca ttcagtatta taatggagaa gagagagcaa aaggaaacat 600  
 tcttgaacga ttctccgcac aacagttccc tgacttgac tctgaactaa acctgagctc 660  
 tctggagctg ggggactcag ctttgtattt ctgtgccagc agcgtagggt gtagcttgaa 720  
 acagttcttc gggccaggga cacggctcac cgtgctaggt aagaaggggg ctccagggtg 780  
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 actgggncat 850

<210> 7  
 <211> 847  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(847)  
 <223> n is a, g, c, or t

<400> 7  
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 actecagaat ccaactgggcc tgtgtgtcag aagacaaaag ttaaccataa ggacacagaag 180  
 aaagcctcct gctgaagcca tcgttggtccc acatgcattt cagggacaag aaatgaagat 240  
 cggagacttt caagttgtgc ccaggactca cctgctccca ggagacaaaa ggccacacag 300  
 cagaggagcc tgaagcccat ggcaggatct cctagcttgg ggctgggtgc tctgtagtaa 360  
 gcattctgaa gttcctaagc tcccttcttc ctgataggag cattgacctg tgatgtcacc 420  
 aactgacat actttccct gcaggccact ccagccact gtactctttg gcaggcctca 480  
 ggttctgcta ctccatgtac tattcctgtc ttgcacaggc cagaagctaa aggtgaggag 540  
 gactgaacac agtaccaaca taaccacatc acaccttact ttcctctgcc cgcctgtcc 600  
 ctgcctgac actgattccc cagcccttgc cccccagcc ccttcacct ccactgcccg 660  
 tgcagcagca gagacactcc ctccctgatg caaactgagg cctctggcac cccaactctt 720  
 tcagggcaat gatagtctgt gcttaactct acatggccag gcccactca gggaattctc 780  
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 tacagac 847

<210> 8  
 <211> 755  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(755)  
 <223> n is a, g, c, or t

<400> 8  
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 caggctagag tgcaaggcca tgatcttggc tcaactgcaac ctccacctcc caggttcaag 180  
 tgattctctt gcctcagcct cccaagtagc tagtattaca gacgcctgcc accacgccg 240  
 gttaattttt gtacttttag tagagacagg ttccaccata ttggccaggc tggctcctaaa 300  
 ctccctgacct caggtgatcc tccctgctca gcctcccaaa gtgctgggat tacaggcatg 360

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agctaccacg tctggcctaa gtgcatgtta cctatactaa caaaaccaca cttctgecte 420
gaatgagaac agtctctga acatcttgcc tctttgectg actcaaagcc tcaggtctaa 480
gcctcccat aatttctagt ctcagcagaa agatcaatga caggagactc tcaggtgat 540
gaaattaacc aattaagtaa cctgggttgg catcctcccg tttgttcacc agctcacctn 600
ctgocacagg tatatccttt ctctcancca tatatgcaca aacccccctnc ccacggnaca 660
catannaana atttggaaga ctanaaaatc aggcanggtg tancncacct tnggggctgg 720
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<210> 9
<211> 839
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)..(839)
<223> n is a, g, c, or t

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<400> 9
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ttctaagtgc aagtttattt ttattttttt tttttttttt gagacagagt ctgctctgt 180
caccaggct agagtgcagt ggcctgatct tggctcactg caacctccac ctcccagggt 240
caagtgatcc tcttgctca gcctccaag tagctagtat tacagacgcc tgccaccacg 300
cccggttaat ttttgtactt ttagtagaga caggtttcac catattggcc aggctggtct 360
caaactcctg acctcagggtg atcctcctgc ctacgctcc caaagtgctg ggattacagg 420
catgagctac cacgtctggc ctaagtgcac gttacctata ctaacaaaac cacacttctg 480
cctcgaatga gaacagtctc ctgaacatct tgccctcttg cctgactcaa agcctcaggt 540
ctaagcctcc ccataatttc tagtctcagc agaaagatca atgacaggag actctecagg 600
tgatgaaatt aaccaattaa gtaacctggg ttggcatcct cccgtttgtt caccagctca 660
cctcctgcc caggatatatc ctttctctca gccatatatg cacaaacccc ctccccacgg 720
cacacataga aanaatttgg aagactagaa aatcaggcna gggnttanca cacctngag 780
ggctggagta tggnanccng ggnccgggan atncatncnn tngaaaactt gactatggg 839

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<210> 10
<211> 829
<212> DNA
<213> Homo sapiens

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<220>  
 <221> misc\_feature  
 <222> (1)..(829)  
 <223> n is a, g, c, or t

<400> 10  
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 agttcagatc gaggtcagga acagatggaa cagggtcgac cggtcgaccg gtcgacccta 180  
 gagaaccatc agatgtttcc aggggtgccc aaggacctga aatgaccctg tgccttattt 240  
 gaactaacca atcagttcgc ttctcgcttc tgttcgcgcg cttctgctcc ccgagctcaa 300  
 taaaagagcc cacaaccct cactcggggc gccagtcctc cgattgactg agtcgcccgg 360  
 gtaccctgtg atccaataaa cctcttgca gttgcatccg acttggtggtc tcgctgttcc 420  
 ttgggagggg ctctctgag tgattgacta cccgtcagcg ggggtcttcc agtagcctt 480  
 cctttgtagc aaagacagac agatggtgat ccaagagata cgcaagaaga ggaccgtgtg 540  
 tgtcatggtt gagctctaaa aaagagaaat cacttggtat gaantgaagg agaggaaaag 600  
 gctgatgtgg atggcctgga agangttcga ttggttacct tggcaccgag cttccttct 660  
 catcctcatn cctccctagt ccttgttctt aaaaanantt ttctttctaa ngtccttcc 720  
 ccctccncaa gggggcacia ggatntttta aaaacncctt tccgggcnta attttaacct 780  
 angatccatc ccagncccggt nccnnttttc nnagattcat ttaaacnng 829

<210> 11  
 <211> 710  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(710)  
 <223> n is a, g, c, or t

<400> 11  
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 attttgcaag gcatggaaaa atacataact gagaatagaa aagttcagat cgaggtcagg 180  
 aacagatgga acagggtcga ccggtcgacc ggtcgaccct agagaaccat cagatgttcc 240  
 cagggtgccc caaggacctg aaatgacct gtgccttatt tgaactaacc aatcagttcg 300  
 cttctcgctt ctgttcgcgc gcttctgctc cccgagctca ataaaagagc ccacaacccc 360  
 tcactcgggg cgccagtcct ccgattgact gagtcgccc ggtaccctg tatccaataa 420

accctcttgc agttgcatcc gacttggtgt ctcgctgttc cttggggaggg tctcctctga 480  
 gtgattgact acccgtcagc ggggggtctt cagtagocct tcctttgtag caaagacaga 540  
 cagatgggtga tccaagagat acgcaagaag aggaccgtgt gtgtaatggg tgagctctaa 600  
 aaagagaaat cacttggtatg gaaatgaagg agaggaaagg ctgatgtgga tggctgggaa 660  
 gaggttcgat gggtaccttg gcanccganc ttcnttntn atncccatcc 710

<210> 12  
 <211> 752  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(752)  
 <223> n is a, g, c, or t

<400> 12  
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 ctcccacttc cttccactca tgtaatgaga ggtgctgatg agtcacagga gaggtagccc 180  
 tagataacca acagactgca aaacggacag tccctggatg tctgagccag tgtttgtgca 240  
 ctgcattgac tggctcctcg tagttttttc ctgtagttgc taaagcctgt aaggctctgtg 300  
 tgatgaatat tttctaacc acatctagaag aacataatgc aagacagaat gaaaaactag 360  
 agaggcagaa acccccaaag taagtagtgg gaaattacca ggtatataat aggtcaagcc 420  
 tgctctgcag gagctcaagg gattgtagca ttcttatccc aaaccactga atcctgggca 480  
 aaaataagaa gtcgcctaata tttagtatta ccagcttccc aaccccgggc attcttcac 540  
 ttactcaagc tgtccagagg cccaggggtg actccctata agtcccatgg gtggctgaga 600  
 tctattttaga ggcacaaggg tatctnctta taagtccaat gggngggctg agatetatga 660  
 gaagcatctt gggggagagt gccntttggc caccagcatg tggmccctna attttncatg 720  
 nnncaactgg nccngggaag gaaaantttt ga 752

<210> 13  
 <211> 749  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(749)  
 <223> n is a, g, c, or t

&lt;400&gt; 13

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cattttgcaa ggcatggaaa aatacataac tgagaataga aaagttcaga tcgagggtcag      180
gaacagatgg aacaggggtcg accgggtcgac cggtcgaccc tagagaacca tcagatgttt      240
ccaggggtgcc ccaaggacct gaaatgaccc tgtgccttat ttgaactaac caatcagttc      300
gcttctcgct tctgttcgcg cgcttctgct ccccgagctc aataaaagag ccacacaacc      360
ctcactcggg gcgccagtcc tccgattgac tgagtcgccc gggtaaccgt gtatccaata      420
aaccctcttg cagttgcacg cgacttgtgg tctcgctgtt ccttgggagg gtctcctctg      480
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acagatggtg atccaagaga tacgcaagaa gaggaccgtg tgtgtaatgg ttgagcttta      600
aaaaangaga aatcacttgg atggaaatga agganaggaa aaggcntgat ntngatngcn      660
gggaaanagg ttccatnggt nctttggnn anccgannct tnccttcctn atccccntnc      720
cntccctann ncnntnnttn ttaaaaaag      749

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&lt;210&gt; 14

&lt;211&gt; 794

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(794)

&lt;223&gt; n is a, g, c, or t

&lt;400&gt; 14

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ttgacgagtt cttctgagcg ggactctggg gttcgaaatg agctagccct taagtaacgc      120
cattttgcaa ggcatggaaa aatacataac tgagaataga aaagttcaga tcgagggtcag      180
gaacagatgg aacaggggtcg accgggtcgac cggtcgaacc tagagaacca tcagatgttt      240
ccaggggtgcc ccaaggacct gaaatgaccc tgtgccttat ttgaactaac caatcagttc      300
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aaccctcttg cagttgcacg cgacttgtgg tctcgctgtt ccttgggagg gtctcctctg      480
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acagatggtg atccaagaga tacgcaagaa gaggaccgtg tgtgtaatgg ttgagctcta      600
aaaaagagaa atcacttggg tggaaatgaa ggagaggaaa aggctgatgt ggatggctgg      660

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gaagagggttc gatggttacc ttggcaaccg agcttccctn ctcattccca tccctnecta 720  
 gtccttggtc tttaaaaaga tttttttnt aatgtccctt nccctccaca agggggcaca 780  
 agatgttttn aaac 794

<210> 15  
 <211> 784  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(784)  
 <223> n is a, g, c, or t

<400> 15  
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 tcaagttctc aatgtatgga tgtcccgcc caggctacca tactccagcc ctcaagggtg 180  
 gctatacctt gcctgatttt ctagtcttcc aaattcttct atgtgtgccg tggggagggg 240  
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 aaacgggagg atgccaaccc aggttactta attggttaat ttcattcacct ggagagtctc 360  
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 agtcaggcaa agaggcaaga tgttcaggag actgttctca ttcgaggcag aagtgtgggt 480  
 ttgttagtat aggtaacatg cacttaggcc agacgtggta gctcatgcct gtaateccag 540  
 cactttggga ggctgaggca ggaggatcac ctgaggtcag gagttttgag accagcctgg 600  
 ccaatatggg ggaaaacctg tctctactaa aaagtacaaa aattaacctg gncgtngng 660  
 gcaggnntc tgtaatacta nntacttgg gngntgnag gcaanaaat cantttgaac 720  
 ctnggnaggg gggngnttgc aatnnccna aaaanatgcc cnntggncct ttaaccntgg 780  
 gngn 784

<210> 16  
 <211> 757  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(757)  
 <223> n is a, g, c, or t

<400> 16



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tttttttttt ttttgagaca gagtctcgct ctgtcaccca ggctagagtg cagtggcatg      180
atcttggttc actgcaacct ccacctccca ggttcaagtg attctcttgc ctacgcctcc      240
caagtagcta gtattacaga cgctgccac cacgccgggt taatttttgt acttttagta      300
gagacagggt tcaccatatt ggccaggctg gtctcaaact cctgacctca ggtgatcctc      360
ctgcctcagc ctcccaaagt gctgggatta caggcatgag ctaccacgtc tggcctaagt      420
gcatgttacc tatactaaca aaaccacact tctgcctcga atgagaacag tctcctgaac      480
atcttgcttc tttgcctgac tcaaagcctc aggtctaagc ctcccataa tttctagtct      540

tgggttggca tcctccggtt tgttcaccag ctcacctnct gncacaggta tatncttttt      660
tctnagccat atatgccaa anccccctnc ccacggnaca catngaagaa nttnngaaga      720
ctngaaaatc aggccagggt tnngccacc ttngggg      757

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<210> 17
<211> 783
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)..(783)
<223> n is a, g, c, or t

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<400> 17
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ttttattttt tttttttttt ttgagacaga gtctcgctct gtcaccagg ctagagtga      180
gtggcatgat cttggctcac tgcaacctcc acctcccagg ttcaagtgat tctcttgct      240
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gcctaagtgc atgttaccta tactaacaaa accacacttc tgccctcgaat gagaacagtc      480
tcctgaacat cttgcctctt tgccctgactc aaagcctcag gtctaagcct ccccataatt      540
tctagtctca gcagaaagat caatgacagg agactctcca ggtgatgaaa ttaaccaatt      600
aagtaacctg ggttggcatc ctccggttg ttcaccagct cacctcctgc cacagggtata      660
tcctttctct cagccatata tgcacaaacc cctnccac ggcacacata gaagaatttg      720

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gaagactaga aaatcaggca nggtatagca caccttggag ggctggagta tggtagcctg 780

ggc

783

<210> 18  
 <211> 770  
 <212> DNA  
 <213> Homo sapiens

<220> "  
 <221> misc\_feature  
 <222> (1)..(770)  
 <223> n is a, g, c, or t

<400> 18  
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 tttttttttt ttgagacaga gtctcgctct gtcacccagg ctagagtgc gtggcatgat 180  
 cttggctcac tgcaacctcc acctcccagg ttcaagtgat tctcttgctt cagcctccca 240  
 agtagctagt attacagacg cctgccacca cgcccggtta atttttgtac ttttagtaga 300  
 gacaggtttc accatattgg ccaggctggg ctcaaactcc tgacctcagg tgatcctcct 360  
 gcctcagcct cccaaagtgc tgggattaca ggcattgagct accacgtctg gcctaagtgc 420  
 atgttaccta tactaacaaa accacacttc tgctcgaat gagaacagtc tcctgaacat 480  
 cttgcctctt tgctgactc aaagcctcag gtctaagcct ccccataatt tctagtctca 540  
 gcagaaagat caatgacagg agactctcca ggtgatgaaa ttaaccaatt aagtaacctg 600  
 gggtggcatc ctcccgtttg ttcaccagct cacctnctgc cacagggtata tcctttttct 660  
 tagccatata tgcacaaacc cccttcccac ggnacacata gaaaaatttn ggaagactag 720  
 aaaatcaggc agggtnntagc acacctngn gggctnggag tntnggtanc 770

<210> 19  
 <211> 774  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(774)  
 <223> n is a, g, c, or t

<400> 19  
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 tttttttttt ttgagacaga gtctcgctct gtcacccagg ctagagtgc gtggcatgat 180

ctgggtcac tgcaacctcc acctcccagg ttcaagtgat tctcttgccct cagcctccca 240  
 agtagctagt attacagacg cctgccacca cgcccgggta atttttgtac ttttagtaga 300  
 gacaggtttc accatattgg ccaggctggg ctcaaaactcc tgacctcagg tgatcctcct 360  
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 atgttaccta tactaacaaa accacacttc tgcctcgaat gagaacagtc tcctgaacat 480  
 cttgcctctt tgcttgactc aaagcctcag gtctaagcct ncccataatt tctagtctca 540  
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 ggttggcatc ctcccgtttg ntcaccagnc tnacctnctg ncacaggnat atnctttnt 660  
 ttnagccata tntgcacaaa cccctnccc acggnacaca tagaaaaant tnggnagact 720  
 ngaaaattca ggnagggnt tagcncnccc ttgggggnt ggnntntngg aacc 774

<210> 20  
 <211> 914  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(914)  
 <223> n is a, g, c, or t

<400> 20  
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 ttgcaaggca tggaaaaata cataactgag aatagaaaag ttcagatcga ggtcaggaac 180  
 agatggaaca gggtcgaccg gtcgaccggt cgaccctaga gaaccatcag atgtttccag 240  
 ggtgccccaa ggacctgaaa tgacctgtg ccttatttga actaaccaat cagttcgctt 300  
 ctcgcttctg ttcgcgcgct tctgctcccc gagctcaata aaagagccca caaccctca 360  
 ctcggggcgc cagtctctcg attgactgag tcgcccgggt aocctgtat ccaataaacc 420  
 ctcttgagcgt tgcattcgac ttgtggtctc gctgttctt gggagggctt cctctgagtg 480  
 attgactacc cgtcagcggg ggtctttcac tctctgtgta ctggtaccaa cagagcctgg 540  
 accagggcct ccagttctc attcagtatt ataatggaga agagagagca aaaggaaaca 600  
 ttcttgaacg attctccgca caacagttcc ctgacttgca ctctgaacta aacctgagct 660  
 ctctggagct gggggactca gcttttgtat ttctgtgcca gcagcgtagg tggtagcttg 720  
 aaacagttct tcngggccag gggacncggc tnaccgggnn aggtaagaag ggggcctcca 780  
 ggtgggaaan aagggtgagc agnccanccc tgcacgaccc nnaaccntn ttcttagggg 840

gaggggnnca ctgggncatn ncagggccnt cntngnggaa nnggggtttg cgccnaggg 900  
ccccagggct gngc 914

<210> 21  
<211> 1604  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)..(1604)  
<223> n is a, g, c, or t

<400> 21  
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catggatcca taacacatag gctagtttac aacaagtaat ttcagcattt ttggataatt 180  
acattccctc cgacaatttc taaggagcct gcatgatact gaactgtgtc agaaaatagg 240  
tgctacagtg aatatgtgat tctaatacagg cttttttact atggaattat agtaaaatgc 300  
actataatca actcatataa attgctctgt gctataactt atctctaattg aaggggaagca 360  
aattgcctta cctgaaatta taaaagaaaa tgattacaaa ggtatggaag tttataggca 420  
tcttataaga cctgatttta ttatgcatta tatagatggc aaaaaattcc tatttatcca 480  
gaatctaaat gaccaggaag ctcaaataaa atgtgtttca tgggaatttg tttttatgtg 540  
ctgaattgca agatcctgaa gggctcttaa gatcatcaaa gaaacatgaa tgctcacaca 600  
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gtgctgagcc caggggagag catggcttgc ccaatgaatt tgtgacaaag cgagacctgg 720  
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tggtattaaa taccacagnc cttttgtgta ttctaantyc ttagaaattt cctaatttat 840  
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tgaaccacag agtaataggc ttattttatt cattcaggga gcttaattta aggtgatcct 1260  
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 cagcaatctg ctttctggga tcatacaagg gaaattgcaa tctttgtgct tgcttgccaa 1440  
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 tcttcctctc acatataacc atcacaaagt aatgcatttc ataatgagaa ganccttgca 1560  
 ctagaagcat acatagtatc acatgmctca tcttctngnt tctn 1604

<210> 22  
 <211> 844  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(844)  
 <223> n is a, g, c, or t

<400> 22  
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 actccagaat ccactgggcc tgtgtgtcag aagacaaaag ttaaccataa ggcacagaag 180  
 aaagcctcct gctgaagcca tcgttggccc acatgcattt cagggacaag aaatgaagat 240  
 cggagacttt caagttgtgc ccaggactca cctgctccca ggagacaaaa ggccacacag 300  
 cagaggagcc tgaagccat gccaggatct cctagcttgg ggctggtgtc tctgtagtaa 360  
 gcattctgaa gttcctaagc tcccttcttc ctgataggag cattgacctg tgatgtcacc 420  
 aactgacat acttccct gcaggccact ccagccact gtactctttg gcaggcctca 480  
 ggttctgcta ctccatgtac tattcctgtc ttgcacaggc cagaagctaa aggtgaggag 540  
 ctgccctgac actgattccc cagcccttgc accccagccc cttaccctc cactgccctg 660  
 gcagcagcag agacactccc tccctgatgc aaactgaggc ctctggcacc cnactcttct 720  
 agggcaatga tagtctgtgc ttaactctac atggccaggc cccactcagg gaattcttat 780  
 gaaattatta tttttttnta tttctgggaa acaaagcgat gtatttattt ctgtttnggg 840  
 gata 844

<210> 23  
 <211> 1562  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature

&lt;222&gt; (1)..(1562)

&lt;223&gt; n is a, g, c, or t

&lt;400&gt; 23

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aaatcccanc aaactgtctc tcagaccaca gtgcaatcaa attagaactc agggttaaga      180
atcacactca aaaccacaca actacatgga aactgaacaa octgctcctg aatgactact      240
gggtaaataa tgaaatgaag gcagaaataa acacgttctt tgaaaccaac tagaacaaag      300
acacaatgta ccagaatctc tgggacacat ttaaagcagt gtgtagaggg aaatttatag      360
cactaaatgc ccacaagaga aagcaggaga gatctaaaat cgacatccta acatcacaat      420
taaaagaact agagaagcaa gagcaaacat attcaaaagc tagcagaaga cgagaadataa      480
ctaagatcag agcagaactg aaggagatag agacacaaaa aaaaccttca aaaattaatg      540
aatgcaggag ctgggtttttt gaaaagatca acaaaatagc cctctagcaa gactaataaa      600
ggataaaaaga gggaagaatc aaatagatgc aataaaaaatg ataaagggga tatcaaccacc      660
aatcccmcmg aaatacaaac taccmtcaga gaatactata aacmcctgta tgcaataaaa      720
ctagaaaatc tagaagaagc agataaatc ctggacacat acaacctccc aagactaaac      780
caggaagaag ttgaatctct gaatagacca ataataggtt ctgaaattga ggcaataatt      840
aatagcctac caaccaaraa aagtcgagga ccagatggat tcacagccgt attctaccag      900
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ggaatcctcc ctaactcatt tatgaggcta gcatcatcct gataccaaag cctggcagag     1020
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ataataagag ctatttatga caaacccata gccaatatca tactgaatgg gcaaaaactg     1380
gaagcattcc ctttgaaaac cagcacaaga caaggatgcc ctctttcacc acttcgatcc     1440
aacctagtat tggaagtctt ggccagggcc atcaagcaag agaaagcaat aaggggtatt     1500
caagtaggaa gagaggggnt ttctgtgtga aaangttanc cgctggnnan ccccaaanan     1560
aa                                                                    1562

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&lt;210&gt; 24

&lt;211&gt; 1446

<212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(1446)  
 <223> n is a, g, c, or t

<400> 24  
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 atcttggggag gagaccattt tgggccttgg ttccacatc tgcgaaatgt tattatagcc 180  
 atgaacactt actgaaagct taccatcatat gccagacaca tcttccaatc aacttatgtg 240  
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 ctccatgtca ccttcaccag agtggtcagg ccattcttca atattcwkac ctrggcaaaa 600  
 ggtgcatgac ttgaactcc cctagttaag ttaaggcttc takaawgaac angannangc 660  
 ttggggagct gaggaagggg gctcactgtg cctataaaa tagagtttca atagacactg 720  
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 atttaaaaaa caaaaaacac aaagacctt ttgtcttaag ctaacttggtg ttgggtttca 1140  
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 tctaaatctt ttantocca ttgctttggg aaagtttcta caccagtnat ccttntacag 1380  
 cctccctctt tccatgggt ctttctctgc accaccagga aaggaggaat cccanancag 1440  
 tcttgc 1446

<210> 25  
 <211> 840  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(840)  
 <223> n is a, g, c, or t

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 agggatgatt gctattctct tcaatgggtt gaggaagaa gaaattatgt gaacatttat 180  
 acactaataa tttattctgt catatttcag tcagattaaa gcaaacagcc aaaaacaagg 240  
 acaaagtcca aggtaagaga ctgatgataa gtggcctgtt tacaaggaaa ataagatcac 300  
 tagctctact tacagctgat tcagaataac ttcattttta aagcctaaaa ttttacagtc 360  
 aagctcttga gtgcaatttc cttaacattt tctaaaccat acagaaaatc ataaagaaac 420  
 aatatttctt tgtttgagtt tcttttttag gagttaggtc ttatttttaa aatattttct 480  
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 tttaccctga ttcagtcagt ttccaaggag aactttgaac aactaaaaat gtgtattact 660  
 ataatctctc tgaaatattn ctnattaatt ttttgggggn aaaatgagtc attctgagcc 720  
 aaaaaaaaaa anggtnacca gacantttcc actnctaact tgnntgggag attnacgcag 780  
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<210> 26  
 <211> 861  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(861)  
 <223> n is a, g, c, or t

<400> 26  
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 acaggaagat gtaggtacct accaatgagc ttacctccc agtgctctat ataacctcac 120  
 ttctatagcc caaagtatta aaaagaagaa aaaataataa ttcaggctta ctatttaaaa 180  
 atacagtgat tctggccggg cacgggtggct cagactgca atcccagcac tttgggaggc 240



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<gagggcgggt ggatcacgtg aggccaggag tttgagacca gcctggccaa tgtgggtgaaa 300
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agctactcgg gaggttgaga tgggagaatt gcttggaccc aggaggcaga gcttgcagtg 420
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gaatctagaa atagcttcan gaantntgga aaagtagatg tgataaaagn tgcatttnaa 780
tcannagaca aagntntaat anaattgaga cacctatgtn gctattngga aacattaang 840
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&lt;210&gt; 27

&lt;211&gt; 875

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(875)

&lt;223&gt; n is a, g, c, or t

&lt;400&gt; 27

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actccagaat ccactgggcc tgtgtgtcag aagacaaaag ttaaccataa ggcacagaag 180
aaagcctcct gctgaagoca tegtgggcc acatgcattt cagggaagaa aaannagat 240
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tgcagcagca gagacactcc ctcttctgat caaactgagg cctctggcac cccaactctt 720
tcagggaat gatagtctgt gcttaactct acatggccag gcccactc aggggaattct 780

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aatatgaatg taaactncag gtgttgncag ctagtgcttc cntggaaaaan cccctgttnc 840  
 agctnctaca catgctctta tctntagctn ganca 875

<210> 28  
 <211> 901  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(901)  
 <223> n is a, g, c, or t

<400> 28  
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 aagttaaact ctgtgagttg aacgcacaca tcacagagca gtttctgaga atgattctgt 240  
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 catgaaaaaa acccgtttcc aacgaaggcc tcaaagaggt caaaatatcc acgtgcagac 480  
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 aacgcacaca tccagagca gtttctgaga aagattctgt ctagttttta taggaaaata 600  
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 agagtgttcc aaatctgctc tgtctaaagg aagggtgaac tctgtgagtt gcatacacac 720  
 aacacaaaga agttactgag aaatcttctg tctagcataa tatgaagaaa tcccgtttcc 780  
 acgaaggcct caagaggnc aatatncaact ggcaggcttn caacagagtg ttntactgc 840  
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 n 901

<210> 29  
 <211> 856  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(856)  
 <223> n is a, g, c, or t

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 gcaaggaaag aaatgcagag gaatggaact gagccatgga acagacattt ggggttgggc 180  
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 gagtgaagtt ttatcataat gaagctaaat gaaattccca aattgctctg gtggagagga 420  
 acgccttgat attccacttg tggaaaaatg gctctatgcc aaaaataaag ttacatcaac 480  
 ctcagtacag gagaaatcag agtttctgct cacagcagca gcagaggaat catctgcaac 540  
 acagagactt ttgggttgta tgtaaggcag ccttgctgga tggctcttaa cagggttttg 600  
 gtagggacat ggtagaggct ggctcctaaa ctcttcaaac gtttcttccc agcccttag 660  
 ctttgacctc acgtgcagag ttgagttaat tataagcctt atttatgggc acactttcac 720  
 cattaagttc atacacagcc ccatttttgt gccattcttc actcctatgt ccttttctcc 780  
 cctaagcaac catgtaaaca tgtagagng gngagcgtg cacacnocat acacacacat 840  
 tcatttacac atgatt 856

<210> 30  
 <211> 890  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(890)  
 <223> n is a, g, c, or t

<400> 30  
 cnnmttctgg gggngtannn aactaannna nntnaatncc nccaatnnn ttcggggggg 60  
 aaancccca gnactccata attcncaagn atcacatgna tcacaggaga ggagactggg 120  
 ggagtcaatg gatagaggat ttataagcca agaaaaaaaa atggagcccc aaactgtgaa 180  
 atccaagaag ggggtcatgt gaacccaat ttatagccag tttttcagaa gaataagtga 240  
 caacctacta cttgtgattg gcacttgaag tgggaggcag tcgtgagggg gttaatatgt 300  
 gggaactaac cctactctag gtagtggtga attgaatcaa atcataggac atctagttgg 360  
 tgtttgctgg aaaactgggt gttggtggag tgaaaccctt acatattttg gtgatcagag 420  
 gtgaagtgtt gtgttaagtg gtatgagact gggaaaaaca ctttggtttt tcctgtctct 480  
 cacagaatta aagtttccaa gagaagcatc agaagagtgg aaggttggga ccagcaaacc 540

```

acaagcccta ggcccaaac tagggtaag tggaaaagca gggataata gtgaaatggc      600
ctctctctcc acttctgcag ctccagtgc gctgttcccta ctcatgtca cactggaatg      660
gttcaggat gaacacgac ctctggaaat ggagacatct tctgaaggta gaggaactg      720
cagtcttct gccccgacc gccactcgca gaggttggga atgtcagcct nctccaacc      780
antctttnt atgggatttt ccttactttg gggggggact gnaatgntac ctatctttt      840
tttacaantt gggggggntc cnceccactt anngaccng ntnnccng      890

```

```

<210> 31
<211> 732
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)..(732)
<223> n is a, g, c, or t

```

```

<400> 31
attcttttgg gnaccgtcag naccaagttt tactcatatc ggcatcctct ctcggtggct      60
gctgcagcgg ggctgggtgtg ctgcaaccgg gacggagctg agtgaggggc acaatggcag      120
caacctgcag gcaccaaaga gccccaaaga gctgctcagc ggtgcctgat caaagtttgt      180
ctgggccagt gcttgtgcat tgtgtacgct gtgcgacaac caggaaggag agctgggttt      240
tgccatcctc caacgcttct taaataggaa actttttggg tagcacctgg cctagtctct      300
ggaacacaga aggtgctgag tgatgttagt ttcattcgct catcttgtct cttgggcag      360
gaaaagagtt tacaagtgtt ctttcattat ccatcttgat gtgggaaggt ggggcagggg      420
aagatgagta cccgctctcg cctttgggtg tgatgtttgt gacgtacatg aggcagtgtg      480
gagagtggat cacagcattg gacagactgg atcocttctg gtccacatc actcaggcaa      540
ctctctcttc ccacctgcc ccctaaactcc cttncacctc cctccacatg tatectccca      600
cttncctcca ctcatgtaat gagaggtgct gatgagtcac aggaagaggt agccctagat      660
aaccaacaga ctgcaaaacg ggacagtncc ntggatgtct gagccagtgt ttngngcact      720
gcattgactg gc      732

```

```

<210> 32
<211> 672
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature

```

&lt;222&gt; (1)..(672)

&lt;223&gt; n is a, g, c, or t

&lt;400&gt; 32

```

tttgnaacc gtcagaccaa gtttactcat atcggatccc aggagacacg ctccaagggc      60
tgggtgggaa aagccccaga aaggggaggg ctgcggggag tgagaatcgg gatggacctc    120
acagacgaca aacagatgga caaaaagctt ctctccctgc cgctccctcc ccgccaccaa    180
ctccagcccc tctgtctcca tccccttttc ctgtctgtcc tgtctgaatc tctgaatctc    240
tgccgtgttn tttttctctc tatgaatcac agcgtttcag agcctctgag agaaaaatgg    300
gaaaagaaga cagagatgat agaaaatgca gagtgtgcgt gtgtgtgtgt gtgtgtgcat    360
gtgtatgcgc gcgtgtgtgt gtgtgtctgt gcatgcgtgc acccagcatg aagtctggtc    420
tggagaatgt aactagggag ggaggaagag aggggacgag agaagcagag gatgaacaaa    480
gagactttcg aagctcatag gaaaaagcct gggaggcaac agcagcaggg acacgcatat    540
gccgcacacc cctacacaca ccacacacca cacaccacac acacctgca tgcacctgg      600
agacatgcc cagactccag gcgggagggg tggagcaggg ggtgtgaaat atggttgggt    660
gggttgggtt tg                                                         672

```

&lt;210&gt; 33

&lt;211&gt; 770

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(770)

&lt;223&gt; n is a, g, c, or t

&lt;400&gt; 33

```

nttttgnant gtnccggnt aacaatttca cacagnaatt cattttaacg ttgtacatat      60
ttattataca agaaatattt tttccatcaa aaagtactca ttcaaaaaat atttaattcta    120
gaatagagat tataaatttt taacttaatt ttattttttt cttaaggaaa actctaagat    180
atcattacca ttttcaaac tgtcaagtag tggatgaatga cacttcttat atgttaattt    240
ttaaagaat atttctaaca cacattctta atggagaatt atatcttata cagaatgata    300
cattctaagg gtgatgttta tgaaagaaat ttaagcttgg ttaacatgct tagtaaaatt    360
ttttaataca aataaaattc agagtatatg gtgtgaagtg agttatatgg tgcaaatact    420
attttaattc tgaacactt ccacaaaatt agcttgtaaa ataaaattaa acccacactg    480
agatgctaga ttgcagatg aatcattcat ttttttacat ttctttttat ttctctaact    540
aaattatatg acagaaggca agggcatga ttaattcatt gttgtattct ttatatatta    600

```

aatataagct cctcaataaa tattatggaa aaaatgaaca aacacttcac attttattgt 660  
 ttcttatatt tttcaaggtt tttattaatt cttcatgtgc ttgtgaott tttttctcc 720  
 aaagaaattc ttcttgaaat gaaaagttca caanagttag gataactgga 770

<210> 34  
 <211> 777  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(777)  
 <223> n is a, g, c, or t

<400> 34  
 nttttgnatt gtngcgcggn taacaatttt cacacagnaa ttcttttgtc aagaattata 60  
 agaagaaatc ccgtttccaa cgaaggcctc aaagagttcc aaatatccac ttgcacactg 120  
 cacaaactaa gtctttccaa actgctctat gcaaagaaat gttcaactct gtgagtttaa 180  
 tacacacatc acaaagcagt ttctgagaat gatactgtct agtttttata cgaagatatt 240  
 tccttttcta ccattggcct catactgcta gaattttcca cttgcaaatt ccacaaaaag 300  
 agtggtttcca atccgctctg tctaaaggaa ggttcaactc tctgatttga atacatacat 360  
 caatataaaa cgtagattgt cacttcaaga aaatacctgc cttatacaga actaagtggc 480  
 tgtttcaagt aaaaatgggtg ttocatgaaa aagctgctag ttcagctggc aactcaaaca 540  
 atggcacaag tgccttatgc catttctatt ttatcacaca tattaaaaac ctggccagca 600  
 cgggtggctca tgcctgtaat tccagcattt tggnaaggcc gaggcagggtg gatcatttga 660  
 ggccagnagt tcaagacang cctggccaac atagcaaac ccccatTTTT actaaaatac 720  
 aaaattagcc aggcntgggg gcgcgtgect gtantccnnc ttctcgggag gctgagg 777

<210> 35  
 <211> 799  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)..(799)  
 <223> n is a, g, c, or t

<400> 35  
 tnnTTTTgga gtgancgagg ntaacaattt tacacaggaa ttctagggtt ggttcatggt 60  
 ttgagacttg agagtggaca ggtgcctagt tagacctgct ctggatgtgg aggtgtctgg 120

```

tgattagaat gactctttgt atatctgttc cctctttaat tgcttccttt taacctcaag      180
attaggcttt tattgcataa taaaatgcat atgagccatt cagttttact ccattacctc      240
tctggcttag aatgaactat cagtagaatt aacaaaaatt gcatcataga gttggagaat      300
tgccaccaag gaagtgttct agccatacta cagaaaagat tctcccatg ggattacttc      360
tcagtagaat tcagcaacca attcctgggtg aatctatcca agcagagaaa tgaaaacata      420
tattcactaa aagacttgaa cacaaatgct catagcagcc ttaatcaaaa tagagaaaaa      480
ctggaaacat ttcaaagtc tatcaactga tcaatatata agcaaatat ataaagcatt      540
tgcagacaat aaaaaacaaa atattgatat atactaaaac atggnatgaa cctcaaagcc      600
actatactag atgagagatg tcagacacaa acctactgta tttgcaagat gccatttact      660
tgaaaaatcc agaaaagtcg catttacaga gacagtaaaa cagataagtg ggctgcctgc      720
ggctgggggg ttgnaaaagc nattttgctg caaatgaact tanggaaatt ttttttgnng      780
ggggggngat anaaaattn                                                    799

```

```

<210> 36
<211> 417
<212> DNA
<213> Canis familiaris

```

```

<220>
<221> misc_feature
<222> (1)..(417)
<223> n is a, g, c, or t

```

```

<400> 36
ancttggtaa ctgtcagnac caagatttac tcatatcgga tccocaggaa tactattctt      60
taaagactat caatattcta caaagggaat ttagagttct caattgtgaa cggaaaggaa      120
catcaatggg catgacctaa gacctcctc tacacagtta aacaacaatt tcacaagata      180
tgatttaaga gaaagctttc agggacgcct ggggtggtca gtggttgagc gtctgccttc      240
cgctcagggg gtgatcctgg agttccggga ctgagtcctc atggggctcc ctgcatggag      300
cctgcttctc cctctgcta tgtctctgcc tctctctgtg tctcatgaat aaataaataa      360
agnncttatt ttttttaaga ttntatttat ttatncatga nagagagaga gaggcng      417

```

```

<210> 37
<211> 434
<212> DNA
<213> Canis familiaris

```

```

<220>
<221> misc_feature
<222> (1)..(434)

```

<223> n is a, g, c, or t

<400> 37

```

tggttaactcg tcagnaccaa gatttactca tatcggcac cccaggaata ctattcttta      60
aagactatca atattctaca aagggaaatt agagttctca attgtgaacg gaaaggaaca      120
tcaatgggca tgacctaga cctccttcta cacagttaaa caacaatttc acaagatatg      180
atttaagaga aagctttcag ggacgcctgg gtggctcagt ggttgagcgt ctgccttcgg      240
ctcaggggtg gatcctggag ttccgggact gagtcccaca tggggctccc tgcattggagc      300
ctgcttctcc ctctgectat gtctctgect ctctctgtgt ctcatgaata aataaataaa      360
gtccttattt tttttaagat tttatttatt tattcatgag agagagagag agncngngnc      420
ntnggcngng ggng                                                         434

```

<210> 38

<211> 1425

<212> DNA

<213> Canis familiaris

<220>

<221> misc\_feature

<222> (1)..(1425)

<223> n is a, g, c, or t

<400> 38

```

cnggncggng angattntng tcgnnaccca tggcgaatgc ctggctngcc gaatattcat      60
gggtggaaaat ggccngcttt tctggattca tcgnactgtg nccggctggg tgtggcggac      120
ccgctatnca gnacatagcg ttgggctacc cngtgataat gctgaagagc ttggcgngcg      180
aatgggctga ccgcttcctc gtgskkkanc ggtatcgccg ctcyccgatt cgcagcgcac      240
cgccttctat cgccttcttg acgagttctt ctgagcggga ctncctggggt tcgaaatgag      300
ctagccctta agtaacgcca ttttgcaagg catggaaaaa tacataactg agaataaaaa      360
agttcatctc tgctgtcttt ggccattctc tctaggcatc tgctcatgtg gaggcataag      420
aaaatattga catgcttcac attacatttt cagagtatgt tattcatgta atttatttgt      480
aaaatctacc aatacaattt cccccaatc aagtaaaact aggtaaaaag atctctgcaa      540
agattagctg aggaagaaac atatgtgagt agaatacaga tgtaagagc tgacaggtta      600
gcagatagca tgcccatgat ttttgtgggt ttggccctt tgttgaagct aaatcttaca      660
gagaggccca accctagagg taaaatgatt aaaacagatg tgctgcagtt ggcggggagg      720
gtgctgcgcc aggggaagcc caagactgct gctggctgcc ttccctectg aycttatccc      780
atgtctcatt tgaaaaccaa tagttgaaaa actctcaatt ttcagatgag aacgaaaaca      840
aaaatgcaaa gaaggcaaat gattcaytca aarwtactca gtgaatkrga sccawsatgt      900

```



```

gggaatacaa ctctggcctt ctgtttctga atctagtggg atttocaggc tcacaggaag      960
cttcctgtac cttgctccac tgtgtgtgtt ttgggatggc cctgggtgtt gattacctyt    1020
cgtggcaggc ccaacagccc ttgctaaggc acagactgca tatttgctga tccctgaggn    1080
ggaaagctgt gattcagact ttgaggtcta agaattgcag acttagtttc tagtctcccg    1140
atgaaactgc taatctgggt gccagtgggt tttctgtac acggacacct gcccacacag    1200
catgattaga aattataatg atgacggcga tgagtcttcc aggacaccta cgttctttgc    1260
aagatatttc tgctaactgt ctctaccaga atcagttgga gaactttttt tagttttttt    1320
tttttttttt taatttcocc ctttctaagt caagtaaaaa tactagttta attnotgggt    1380
tagggtaatg atttgtctc accattactg atgtgtcatt ttttg                      1425

```

```

<210> 39
<211> 674
<212> DNA
<213> Canis familiaris

```

```

<220>
<221> misc_feature
<222> (1)..(674)
<223> n is a, g, c, or t

```

```

<400> 39
caaaaaatga cacatcagta atggtgagga caaatcatta ccctacacca gnaattaaac      60
tagtatTTTT acttgactta gaaaggggga aattaaaaaa aaaaaaaaaa aactaaaaaa    120
agttctccaa ctgattctgg tagagacgat tagcagaaat atcttgcaaa gaacgtaggt    180
gtcctggaag actcatcgcc gtcatcatta taatttctaa tcatgctgtg tgggcagggt    240
tccgtgtagc agaaacacca ctggcaccca gattagcagt ttcacggga gactagaaac    300
taagtctgca attcttagac ctcaaagtct gaatcacagc tttccctca gggatcagca    360
aatatgcagt ctgtgcctta gcaagggctg ttgggocctg cagcagaggt aatcaaacac    420
cagggccatc caaaaacaca cacagtggag caaggtagag gaagcttcct gtgagcctgg    480
aaataccact agattcagaa acagaaggcc agagtgtgat toccacatga tggctctaata    540
tcactgagta actttgaatg aatcatttgc cttctttgca tttttgtttt cgttctcatc    600
tgaaaaattga gagtttttca actattgggt ttcaaatgag acatgggata agatcaggag    660
ggaaggcagc cagc                                                         674

```

```

<210> 40
<211> 666
<212> DNA
<213> Canis familiaris

```

<220>  
 <221> misc\_feature  
 <222> (1)..(666)  
 <223> n is a, g, c, or t

<400> 40  
 cccatgagca aaaaatgaca catcagtaat ggtgaggaca aatcattacc ctacaccagn 60  
 aattaaacta gtattttttac ttgacttaga aagggggaaa ttaaaaaaaaaa aaaaaaaaaa 120  
 ctaaaaaaaaag ttctocaact gattctggta gagacgatta gcagaaatat cttgcaaaga 180  
 acgtagggtgt cctggaagac tcatcgccgt catcattata atttctaatac atgctgtgtg 240  
 ggcagggtgtc cgtgtagcag aaacaccact ggcacccaga ttagcagttt catcgggaga 300  
 ctagaaacta agtctgcaat tcttagacct caaagtctga atcacagctt tcccctcagg 360  
 gatcagcaaa tatgcagtct gtgccttagc aagggtgtgtt gggcctgccca cgagaggtaa 420  
 tcaaacacca gggccatcca aaaacacaca cagtggagca aggtacagga agcttcctgt 480  
 gagcctggaa ataccactag attcagaaac agaaggccag agttgtattc ccacatgatg 540  
 gctctaattc actgagtaac tttgaatgaa tcatttgcct tctttgcatt tttgttttcg 600  
 ttctcatctg aaaattgaga gtttttcaac tattgggtttt caaatgagac atgggataag 660  
 atcagg 666

<210> 41  
 <211> 603  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> misc\_feature  
 <222> (1)..(603)  
 <223> n is a, g, c, or t

<400> 41  
 cccatgagca aaaaatgaca catcagtaat ggtgaggaca aatcattacc ctacaccaga 60  
 attaaactag tattttttact tgacttagaa aggggggaaat taaaaaaaaa aaaaaaaac 120  
 taaaaaaaaagt tctccaactg attctggtag agacgattag cagaaatatc ttgcaaagaa 180  
 cgtaggtgtc ctggaagact catcgccgtc atcattataa tttctaatac tgctgtgtgg 240  
 gcagggtgtc gtgtagcaga aacaccactg gcacccagat tagcagtttc atcgggagac 300  
 tagaaactaa gtctgcaatt cttagacctc aaagtctgaa tcacagcttt cccctcaggg 360  
 atcagcaaat atgcagtctg tgccttagca aggggtgttg ggectgccac gagaggtaat 420  
 caaacaccag ggccatccaa aaacacacac agtggagcaa ggtacaggaa gcttcctgtg 480

agcctggaaa taccactaga ttcagaaaca gaaggccaga gttgtattcc cacatgatgg 540  
 ctctaattca ctgagtaact ttgaatgaat catttgcctt ctttgcattt ttgttttcgt 600  
 tct 603

<210> 42  
 <211> 749  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> misc\_feature  
 <222> (1)..(749)  
 <223> n is a, g, c, or t

<400> 42  
 ggnactgtn cgnaccagtt tactncatat nccgntnccc atgagcaaaa aatgacacat 60  
 cagtaatggt gaggacaaat cattacccta caccagnaat taaactagta tttttacttg 120  
 acttagaaag ggggaaatta aaaaaaaaaa aaaaaaacta aaaaaagttc tccaactgat 180  
 tctggtagag acgattagca gaaatatctt gcaaagaacg taggtgtcct ggaagactca 240  
 tcgccgtcat cattataatt tctaatactg ctgtgtgggc aggtgtccgt gtagcagaaa 300  
 caccactggc acccagatta gcagtttcat cgggagacta gaaactaagt ctgcaattct 360  
 tagacctcaa agtctgaatc acagctttcc cctcagggat cagcaaatat gcagtctgtg 420  
 ccttagcaag ggctgttggg cctgccacga gaggtaatca aacaccaggg ccatccaaaa 480  
 acacacacag tggagcaagg tacaggaagc ttcctgtgag cctggaaata ccactagatt 540  
 cagaaacaga aggccagagt tgtattccca catgatggct ctaattcact gagtaacttt 600  
 gaatgaatca ttgtccttct ttgcattttt gttttcggtc tcatctgaaa attgagagtt 660  
 tttcaactat tgggtttcaa atgagacatg ggataagatc aggagggaag gcagccagca 720  
 gcagtcttgg gcttcccctg ggcagcac 749

<210> 43  
 <211> 1778  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> misc\_feature  
 <222> (1)..(1778)  
 <223> n is a, g, c, or t

<400> 43  
 gkggtagn gnrcggtaaaca atttncacac agcaattnc cctgtgnaaa ctgccttgac 60  
 ttggtgcctt ttttgagggt gtggagtgtg ttocactttg acaaattttt atattctcc 120

catcctaatt ggactaatct gcttttatat ctcttctgtg gttattttgt taatcgtatt 180  
 ttaggaaagt cacctatttc aaattgattt gcatggagct aaataatttc ttccaatttt 240  
 ttcatttctt ttgtgtttat ggttatttct acattattag tgaaagtttt gtgggtttgt 300  
 gtttttagttc tctatctctt cttttgatta gtttcacaga gtttagttgt tattttttca 360  
 gaaaacagct cttgcactta tttatcggct ctactgttct taatttgctc ctaaaaattg 420  
 tcaataatat gtttcttttg ctttgccggg gctcattttg ttgtttttct aattgtttga 480  
 gcttgactct taattcatct atttttgttt ctgctttttt gttaatgtaa atttaaaaaa 540  
 tgcgagatcc aattagaata agcctcaccg gacaagaacc tgtctgtgca cttcgagact 600  
 accataatgc ctatcacata gcagggtgctt aagcaaaatt tttgtatgaa taaataaacc 660  
 cctatgaaat aattatggga tttgtgtgac agcctcgtt ctctctgtct gtctttggsc 720  
 aytctctcta ggcatctgct catgtggagg cataagaaaa tattgacatg cttcacatta 780  
 cattttcaga gtatgttatt catgtattta tttgtaaaat ctaccaatac aatttcccc 840  
 caatcaagta aaactaggta aaaagatctc tgcaaagatt agctgaggaa gaaacatatg 900  
 tgagtaraat caraatgtta agagctrmca gggtarcaga tagcatgcc atgatttttg 960  
 tgggkttggc ccttttggtg aagctaaatc ttacagagag gcccaacct agaggtaaaa 1020  
 tgattaaaac agatgtgctg cagttggcgg ggagggtgct gcgccarggg aagncccaag 1080  
 actgtgctg gctgccttcc ctccntgatc ttatcccatg tctcatttga aaaccaatag 1140  
 ttgaaaaact ctcaattttc agatgagaac gaaaacaaaa atgcaaagaa ggcaaatgat 1200  
 tcattcaaag ttactcagtg aattagagcc atcatgtggg aatacaactc tggccttctg 1260  
 tttctgaatc tagtggtatt tccaggctca caggaagctt cctgtacctt gctccactgt 1320  
 gtgtgttttt ggatggccct ggtgtttgat tacctctctg ggcaggccca acagcccttg 1380  
 ctaaggcaca gactgcatat ttgctgatcc ctgaggggaa agctgtgatt cagactttga 1440  
 ggtctaagaa ttgcagactt agtttctagt ctcccgatga aactgctaat ctgggtgcca 1500  
 gtgggtgttc tgctacacgg acacctgcc acacagcatg attagaaatt ataatgatga 1560  
 cggcgatgag tcttccagra cacctacgtt ctttgcaaga watttctgct aatcgnntnc 1620  
 tctaccagaa tcagttggag aacttttttt agtttttttt tttttttttt aatttcccc 1680  
 tttctaagtc aagtaaaaaat actagtttaa ttctgggtga gggtaatgat ttgtcctcac 1740  
 cattacttga aagaccccac ctgtagggtg gcaagcgg 1778

<210> 44  
 <211> 868  
 <212> DNA

<213> Canis familiaris

<220>

<221> misc\_feature

<222> (1)..(868)

<223> n is a, g, c, or t

<400> 44

```

tbcctgagac ngcttgccaa acctacaggt ggggtctttc aagtaatggt gaggacaaat      60
cattacecta caccagaatt aaactagtat ttttacttga cttagaaagg gggaaattaa      120
aaaaaaaaa aaaaaactaa aaaaagttct ccaactgatt ctggtagaga cgattagcag      180
aaatatcttg caaagaacgt aggtgtcctg gaagactcat cgccgtcctc attataattt      240
ctaatacatgc tgtgtgggca ggtgtccgtg tagcagaaac accactggca ccagattag      300
cagtttctac gggagactag aaactaagtc tgcaattctt agacctcaa gtctgaatca      360
cagctttccc ctcagggatc agcaaatacg cagtctgtgc cttagcaagg gctgttgggc      420
ctgcccagag aggtaatcaa acaecagggc catccaaaaa cacacacagt ggagcaaggt      480
acaggaagct tctgtgagc ctggaaatac cactagattc agaaacagaa ggccagagtt      540
gtattcccac atgatggctc taattcactg agtaactttg aatgaatcat ttgccttctt      600
tgcatttttg ttttcgttct catctgaaaa ttgagagttt ttcaactatt ggttttcaaa      660
tgagacatgg gataagatca ggagggaagg cagccagcag cagtcttggg ctccctggc      720
gcagcacent cccgccaact gcagcacatc tgtttaatca tttaacctct aggnntgggcc      780
tttctgtaag atttagcttn acaangggcc aaacccaaaa aatcatgggc atgcttctgc      840
tacctgnca ntaacattt gatntac      868

```

<210> 45

<211> 1237

<212> DNA

<213> Canis familiaris

<220>

<221> misc\_feature

<222> (1)..(1237)

<223> n is a, g, c, or t

<400> 45

```

ggtatcgccg ctcccgatc gcaccgcac gccttctatc gccttcttga cgagttcttc      60
tgagcgggac tctgggggtc gaaatgagct agcccttaag taacgccatt ttgcaaggca      120
tggaaaaata cataactgag aatagaaaag ttcattctctg ctgtcttttg ccattctctc      180
taggcattctg ctcatgtgga ggcataagaa aatattgaca tgcttcacat tacattttca      240
gagtatgtta ttcatgtatt tatttgtaaa atctaccaat acaattcccc ccaatcaag      300

```

```

taaaactagg taaaaagatc tctgcaaaga ttagctgagg aagaaacata tgtgagtaga      360
atcagaatgt taagagctga caggtagca gatagcatgc ccatgatttt tgtgggtttg      420
gccctttgt tgaagctaaa tcttacagag aggcccaacc ctagaggtaa aatgattaaa      480
acagatgtgc tgcagttggc ggggaggggtg ctgcgccagg ggaagcccaa gactgctgct      540
ggctgccttc cctcctgac ttatcccat gtctcatttg aaaaaccaat agttgaaaaa      600
ctctcaattt tcagatgaga acgaaaacaa aaatgcaaag aaggcaaatg attcattcaa      660
agttactcag tgaattagag ccatcatgtg ggaatacaac tctggccttc tgttcttgaa      720
tctagtggta ttccaggct cacaggaagc ttcctgtacc ttgctccact gtgtgtgttt      780
ttggatggcc ctgggtgttg attacctctc gtggcaggcc caacagocct tgctaaggca      840
cagactgcat atttgctgat ccctgagggg aaagctgtga ttcagacttt gaggtctaag      900
aattgcagac ttagtttcta gtctcccgat gaaactgcta atctgggtgc cagtgggtgt      960
tctgctacac ggacacctgc ccacacagca tgattagaaa ttataatgat gacggcgatg     1020
agtcttcag gacacctacg tcttttgcaa gatatttctg ctaatcgtct ctaccagaat     1080
cagttggaga acttttttta gttttttttt ttttttttta atttccccct ttctaagtca     1140
agtaaaaata ctagtttaat tctgggtgtg ggtaatgatt tgcctcacc attactgatg     1200
tgtcattttt tgcctatggg atccgatatg agtaaac                                1237

```

<211> 703  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> misc\_feature  
 <222> (1)..(703)  
 <223> n is a, g, c, or t

```

<400> 46
ccctgtgaaa ctgccttgac ttggtgcctt ttttgagggt gtggagttgt ttccactttg      60
acaaattttt atatttctcc catcotaatt ggactaattt gcttttatat ctcttctgtg     120
gttattttgt taatcgtatt ttaggaaagt cacctatttc aaattgattt gcatggagct     180
aaataatttc ttccaatttt ttcatttcct ttgtgtttat ggttatttct acattattag     240
tgaaagtttt gtggttttgt gttttagttc tctatctcct cttttgatta gtttcacaga     300
gtttagttgt tattttttca gaaaacagct cttgcactta tttatcggct ctactgttct     360
taatttgctc ctaaaaattg tcaataatat gtttcttttg ctttgcccggt gctcattttg     420
ttgtttttct aattgtttga gcttgactct taattcatct attttgtttt ctgctttttt     480

```

gttaatgtaa atttaaaaaa tgcgagatcc aattagaata agcctcaccg gacaagaacc 540  
 tgtctgtgca cttcgagact accataatgc ctatcacata gcagggtgctt aagcaaaatt 600  
 ttgtatgaa taaataaacc cctatgaaaa aattatggga ttgtgtgac agccctcggt 660  
 cttctctgct gnccttgccc attctctcta ggcctctgct cat 703

<210> 47  
 <211> 304  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> misc\_feature  
 <222> (1)..(304)  
 <223> n is a, g, c, or t

<400> 47  
 ctagcttgcc aaacctacag gtggggtctt tcaagtaatg gtgaggacaa atcattaccc 60  
 tacaccagaa ttaaaactagt atttttactt gacttagaaa gggggaaatt aaaaaaaaaa 120  
 aaaaaaact aaaaaaagtt ctccaactga ttctggtaga gacgattagc agaaatatct 180  
 tgcaaagaac gtaggtgtcc tggaagactc atcgccgtca tcattataat ttctaatacat 240  
 gctgtgtggg cagggtgtccg tgtagcagaa acaccactgg nccccagat nagagttttc 300  
 ttgg 304

<210> 48  
 <211> 735  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> misc\_feature  
 <222> (1)..(735)  
 <223> n is a, g, c, or t

<400> 48  
 agcttgccaa acctacaggt ggggtctttc aagtaatggt gaggacaaat cattacccta 60  
 caccagaatt aaactagtat ttttacttga cttagaaagg gggaaattaa aaaaaaaaaa 120  
 aaaaaactaa aaaaagtctt ccaactgatt ctggtagaga cgattagcag aaatatcttg 180  
 caaagaacgt aggtgtcctg gaagactcat cgccgtcatc attataatct ctaatacatgc 240  
 tgtgtgggca ggtgtccgtg tagcagaaac accactggca ccagattag cagtttcatc 300  
 gggagactag aaactaagtc tgcaattctt agacctcaaa gtctgaatca cagctttccc 360  
 ctcagggatc agcaaatatg cagtctgtgc cttagcaagg gctgttgggc ctgccacgag 420  
 aggtaatcaa acaccagggc catccaaaaa cacacacagt ggagcaaggt acaggaagct 480

tctgtgagc ctggaaatac cactagattc agaaacagaa ggocagagtt gtattcccac 540  
 atgatggctc taattcactg agtaactttg aatgaatcat ttgccttctt tgcatttttg 600  
 ttttcgttct catctgaaaa ttgagagttt ttcaactatt ggttttcaaa tgagacatgg 660  
 gataagatca ggaggggaagg cagccagcag cagtcttggg ctttccctgg cgcaaaacn 720  
 tccccgcaac tggag 735

<210> 49  
 <211> 1412  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> misc\_feature  
 <222> (1)..(1412)  
 <223> n is a, g, c, or t

<400> 49  
 cttccccact nnnaccntg gncettaaca gncacnnnc tttggagata gctaactcct 60  
 acncattcaa catcagtgn anggnctctc tccagaaggc ttcctcnacc ctttcaattc 120  
 ccacttacnt gtaagcctag gatgcctcct ctcagattca gactgggtgn cncagtgttt 180  
 aagaacttna gctgtacagc canagagttt gtattggaaa ataactcttg tggttttttg 240  
 tcngcatgat cttggacgag ttattttaacc cctcagnt agtttcttca tccatataat 300  
 ctggcaaatg atagtncnca gtccatacaa ttgtnagcac taaacaaaat aatgtacacg 360  
 agcctggcac actgaaggan cccagtgaag ggtggtgtg attactnaca gtccttctca 420  
 ttctctagca tagcacttac cgtgttgctg tccgattttc tgtctgcatg tctacctgca 480  
 tgtcgggttg catgcagact atgaactgga agctgaatcc ccagtgcctg gtacaatgtg 540  
 agaccccata ncagttcatt gaatgaattc agacacttca gtttttccat aaatttcagc 600  
 cttcttcaat attttgctcc tattttctag aagtttctga aagagcagct tggaaatgt 660  
 cagcaatttc taatttctta gcttttcagt gtgtgtgctg gtgtgtgctg gtgtgttga 720  
 tattttctgc tgtggaaacc gctggactta gatgatcagn ctgtgagata caggcaggac 780  
 anagataaga agtaggagga gggctncgat gatgaagctt aggcactgaa gcaactcagc 840  
 caccaccag gaagcctcag tncctgaar aggtggacc tkkcasscyg wggatgaacca 900  
 ttgtgggcca aagaggcca gtgcatgcat gaggcagacc tccctctaca gggaggcttt 960  
 gccctactgg gatttatttc cttgctgctt aaggacctgg ctttgctcct gcctttcctt 1020  
 gtcccttca tctgattctc tggccttatt ttggccagca gattgcaatt gcctgtccag 1080  
 ttaacatat aaatgcattc tctcctcat gacctcttct cagcctgctg gtctaaggga 1140



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ggagctctgt ttcttgatcc tgcctctga ctaaattttc tcttgctgt cttccctttc 1200
ctgatgattc agtacagaca cctgccaat tccacttttt ctcttcattt ccaattattt 1260
gggtggtcaag actgtttact caaatatgca tctggtttta tcacgagcca cgactctgac 1320
taaagtagcc tgattatatg gttctttaag ggatagctga ctttcacaaa cctaagaaaa 1380
gttncctaaa gtggtgttct aagggnccca ca 1412

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```

<210> 50
<211> 866
<212> DNA
<213> Canis familiaris

```

```

<220>
<221> misc_feature
<222> (1)..(866)
<223> n is a, g, c, or t

```

```

<400> 50
ttnnnggacn gcttgccaaa cctacaggtg gggctcttca agatctgctg acagtgaagc 60
taaactctggc ggaagcaaag gattcacttt ctcataatgg attaactcat cctatttgcc 120
tcttaaacaa tgggtatttt aaagacagaa gttgaaggaa gtccaagtat ccaattttta 180
ggatgcctat tagagcagtt ataagagagt gtctctcttt ctctctcttc tttctctctc 240
ttggtaggag tatgcaggag gtcattttaa agccagatag tgatacaaat cacaatgcag 300
aaaaacatcc ccgtggactc ctccctgtcc tatgtttgac attcttaaaa tctatgtccc 360
aggctctgaa atcttttaaat aatctaccat gttcttttggc ctgccctggg aaatctattt 420
cagtaccaga gctatgctgg ttacacacct tttctgactc atgttcccaa gtgattttat 480
cccagatagc atttggggac agttacgtgt actgttctga tatcttctta aaaggaaatt 540
atthttggaag taaagtcact gataaaatca actcaggaaa atgcactttg taaatattaa 600
aatataaaca ttattaaagg ccatgctgta aaaatactaa ttgattttcc tgtgtagcag 660
ttacaataga acaacgatag atctctaagg ggagagtgaaggaggacctcaa ttgagaaac 720
gtgaggcagg aaaagtttca aataattata ttcagagtgn tacctaagtt gttacttaaa 780
gacattctct acgtaaaana aacaataagg ccaaataagc gaatgagagt tatgttatcg 840
cagaaacaan gtaancggnt tntttt 866

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<210> 51
<211> 597
<212> DNA
<213> Canis familiaris

```

<220>  
 <221> misc\_feature  
 <222> (1)..(597)  
 <223> n is a, g, c, or t

<400> 51  
 acacagcaat tcattncaat gaactgttat ggggtctcac attgtaccag gcactgggga 60  
 ttcagcttcc agttcatagt ctgcatgcaa aocgacatgc aggtagacat gcagacagaa 120  
 aatcggaacg caacacggta agtgctatgc tagagaatga gaaggactgt cagtaatcac 180  
 aaccaecttt cactgggttc cttcagtgtg ccaggctcgt gtacattatt ttgttttagtg 240  
 ctccacaattg tatggactgt gtactatcat ttgccagatt atatggatga agaaactaga 300  
 ctgaggggggt taaataactc gtccaagatc atgcagacaa aaaaccacag agattatatt 360  
 ccaatacaaa ctctctggct gtacagctca agttcttaaa cactgggcca accagtctga 420  
 atctgagagg aggcattcta aggccttacag gtaagtggga attgaaaggg ttgaggggaag 480  
 ccttctggag gagatgccat tacactgaat gttgaatgag taggagttag ctatctecag 540  
 aggggtagtg gctgtgaagg ggcgaggggt agagggtggg aaggggatga tggaagg 597

<210> 52  
 <211> 875  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> misc\_feature  
 <222> (1)..(875)  
 <223> n is a, g, c, or t

<400> 52  
 cgcttgccaa cctacagggtg gggctcttca agatctgctg acagtgaagc taaatctggc 60  
 ggaagcaaag gattcacttt ctcataatgg attaaactcat cctatttgcc tcttaaacaa 120  
 tgggtatattt aaagacagaa gttgaaggaa gtccaagtat ccaattttaa ggatgcctat 180  
 tagagcagtt ataagagagt gtctctcttt ctctctcttc tttctttctc ttggtaggag 240  
 tatgcaggag gtcattttaa agccagatag tgatacaaat cacaatgcag aaaaacatcc 300  
 ccgtggactc ctccctgtcc tatgtttgac attcttaaaa tctatgtccc aggtcttgaa 360  
 atctttaaat aatctaccat gttctttggc ctgccctggg aaatctattt cagtaccaga 420  
 gctatgctgg ttacacacct tttctgactc atgttcccaa gtgattttat tccagatagc 480  
 atttggggac agttacgtgt actgttctga tatcttcta aaaggaaatt attttggaag 540  
 taaagtcact gataaaatca actcaggaaa atgcactttg taaatattaa aatataaaca 600  
 ttattaaagg ccatgctgta aaaatactaa ttgattttcc tgtgtagcag ttacaataga 660

acaacgatag atctctaagg ggagagtgaaggacctcaa ttgagaaac gtgaggcagg 720  
 aaaagtttca aataattata ttcaagagtg ttacctaatg tggtaactta agacattttc 780  
 tacgtaaaat aaacacataa ggccaaanga agggaatgag anttangtta tngcaggana 840  
 aaaggtaaatt cggntttttt ttgtatccat tgcaa 875

<210> 53  
 <211> 612  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> misc\_feature  
 <222> (1)..(612)  
 <223> n is a, g, c, or t

<400> 53  
 agcggataac aatttcacac agnaattcat tcaatgaact gttatggggt ctcacattgt 60  
 accaggcact ggggattcag cttccagttc atagtctgca tgcaaaccga catgcaggta 120  
 gacatgcaga cagaaaatcg gaacgcaaca cggtaagtgc tatgctagag aatgagaagg 180  
 actgtcagta atcacaacca cctttcactg ggttccttca gtgtgccagg ctctgtgtaca 240  
 ttattttgtt tagtgctcac aattgtatgg actgtgtact atcatttgcc agattatatg 300  
 gatgaagaaa ctagactgag ggggttaaata aactcgtcca agatcatgca gacaaaaaac 360  
 cacagagatt attttccaat acaaactctc tggctgtaca gctcaagttc ttaaactctg 420  
 ggccaaccag tctgaatctg agaggaggca ttctaaggct tacaggtaag tgggaattga 480  
 aaggggttgag ggaagccttc tggaggagat gccattacac tgaatgttga atgagtagga 540  
 gttagctatc tccagagggg tagtggctgt gaaggggcga ggggtagagg gtggnaaggg 600  
 atgatngaaa gg 612

<210> 54  
 <211> 732  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> misc\_feature  
 <222> (1)..(732)  
 <223> n is a, g, c, or t

<400> 54  
 agcttgccaa acctacaggt ggggtctttc aagatctgct gacagtgaag ctaaactctgg 60  
 cggaagcaaa ggattcactt tctcataatg gattaactca tcttatttgc ctcttaaaca 120  
 atgggtattt taaagacaga agttgaagga agtccaagta tccaatttta aggatgccta 180

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ttagagcagt tataagagag tgtctctctt tctctctctt ctttctctct cttggttagga      240
gtatgcagga ggtcatttaa aagccagata gtgatacaaa tcacaatgca gaaaaacatc      300
cccgtggact cctccctgtc ctatgtttga cattcttaaa atctatgtcc caggtcttga      360
aatcttttaa taatctacca tgttctttgg cctgccctgg gaaatctatt tcagtaccag      420
agctatgctg gttacacacc ttttctgact catgttcnca agtgatttta ttccagatac      480
gatttgggga cagttacgtg tactgttctg atatcttccct aaaaggaaat tattttggaa      540
gtaaagtcac tgataaaatc aactcaggaa aatgcacttt gtaaataatta aaatataaac      600
attattaaag gccatgctgt aaaaaactaa ttgattttcc tgtgtagcag ttacaataga      660
acacgatgat ctctaagggg agagtgaag gaccttattt ggtaaccgtg aggcagnaaa      720
gtttcaaata tt                                                                732

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<210> 55
<211> 697
<212> DNA
<213> Canis familiaris

```

```

<220>
<221> misc_feature
<222> (1)..(697)
<223> n is a, g, c, or t

```

```

<400> 55
ctagcttgcc aaacctacag gtggggtctt tcaagatctg ctgacagtga agctaaatct      60
ggcggaagca aaggattcac tttctcataa tggattaact catcctattt gcctcttaaa      120
caatgggtat tttaaagaca gaagttgaag gaagtccaag tatccaattt taaggatgcc      180
tattagagca gttataagag agtgtctctc tttctctctc ttctttcttt ctcttggtag      240
gagtatgcag gaggtcattt aaaagccaga tagtgataca aatcacaatg cagaaaaaca      300
tcocgtgga ctctccctg tctatgttt gacattctta aaatctatgt ccaggtctt      360
gaaatcttta aataatctac catgttcttt ggccctgccct gggaaatcta tttcagtacc      420
agagctatgc tggttacaca ccttttctga ctcatgttcc caagtgattt tattccagat      480
acgatttggg gacagttacg tgtactgttc tgatatcttc ctaaaaggaa attattttgg      540
aagtaaagtc actgataaaa tcaactcagg aaaatgcact ttgtaaatat taaaatataa      600
acattattaa aggccatgct gtaaaatact aattgatttt cctgtgtagc agttacaata      660
gaacacgata gatctctang gggagagtga aaggact                                  697

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```

<210> 56
<211> 617

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<212> DNA  
 <213> *Canis familiaris*

<220>  
 <221> misc\_feature  
 <222> (1)..(617)  
 <223> n is a, g, c, or t

<400> 56  
 tggattgcga gcggataaca atttcacaca gaattcattc aatgaactgt tatgggggtct 60  
 cacattgtac caggcactgg ggattcagct tccagttcat agtctgcatg caaaccgaca 120  
 tgcaggtaga catgcagaca gaaaatcgga acgcaacacg gtaagtgcta tgctagagaa 180  
 tgagaaggac tgtcagtaat cacaaccacc ttctactggg ttcttctcagt gtgccaggct 240  
 cgtgtacatt attttgttta gtgctcacia ttgtatggac tgtgtactat catttgccag 300  
 attatatgga tgaagaaact agactgaggg ggtaaataa ctctgccaag atcatgcaga 360  
 caaaaaacca cagagattat ttccaatac aaactctctg gctgtacagc tcaagttctt 420  
 aaacactggg ccaaccagtc tgaatctgag aggaggcatt ctaaggctta caggtaagt 480  
 ggaattgaaa ggggtgaggg aagccttctg gaggagatgc cattacactg aatgttgaat 540  
 gagtaggagt tagctatctc cagaggggta gtggctgtga aggggcgagg ggtagagggt 600  
 ggnaagggga tgaattg 617

<210> 57  
 <211> 803  
 <212> DNA  
 <213> *Canis familiaris*

<220>  
 <221> misc\_feature  
 <222> (1)..(803)  
 <223> n is a, g, c, or t

<400> 57  
 cctgcagcta gcttgccaaa cctacaggtg gggctcttca agatctgctg acagtgaagc 60  
 taaatctggc ggaagcaaag gattcacttt ctcataatgg attaaactat cctatttgcc 120  
 ccttaaacia tgggtatttt aaagacagaa gttgaaggaa gtccaagtat ccaattttaa 180  
 ggatgcctat tagagcagtt ataagagagt gtctctcttt ctctctcttc tttcttctc 240  
 ttggtaggag tatgcaggag gtcatttaaa agccagatag tgatacaaat cacaatgcag 300  
 aaaaacatcc ccgtggactc ctccctgtcc tatgtttgac attcttaaaa tctatgtccc 360  
 aggtcttgaa atcttttaaa aatctaccat gttctttggc ctgccctggg aaatctattt 420  
 cagtaccaga gctatgctgg ttacacacat ttcttgactc atgttcccaa gtgattttat 480

tccagatagc atttggggac agttaagtggt actgttctga tatottccta aaaggaaatt 540  
 attttggaag taaagtcact gataaaatca actcaggaaa atgcactttg taaatattaa 600  
 aatataaaca ttattaaagg ocatgctgta aaaatactaa ttgattttcc tgtgtagcag 660  
 ttacaataga acaacgatag atctctaagg ggagagtgaaggaggacctaa ttgagaaac 720  
 gtgaggcagg aaaagtttca aatattatat tcaagagtgt acctaaagtg ttacttaaag 780  
 acaattctnc acttaaataa acc 803

<210> 58  
 <211> 786  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> misc\_feature  
 <222> (1)..(786)  
 <223> n is a, g, c, or t

<400> 58  
 gngnggnaat gtgcagncgg ntaacaattt cacacagnaa ttccatttcc ctcaacaagc 60  
 aggagaaatt ttctcaagag ttaccagaa gtcactctta acgtcaggct tgcaaatattt 120  
 aaaaagcatg aaaaagaacg tctactacat aatcctccag gcacattcca acacgtgcc 180  
 aacagtattc ctgaaaatcc tctgtcaaac cctccataa atcatagcct cagagctctg 240  
 tgtgtgtggc tgcagcaggc tcgtagctgc agagcacttg catggaggag acatgcgctc 300  
 aggaactgca ccgccgcatt ccgcagaagc cagcgcactt acttccctct gctgcatggt 360  
 aacctgtgct atgttctaga tcttacttta gttagtaatt caacaacagg agtcatgtgg 420  
 gctggcaagt agtcagctga aaactaacat gtgaacagaa ctctcagggg caggcctcca 480  
 gcaagctccc acccgagtca gtactgctcc cgccttcctt tcagcttggt ggtgggtact 540  
 accttctgaa gcctcacaaa accccatctt gaaagaagag gaaactgaga cacggtgaga 660  
 catggtgccc ctgcgccaaa gtctgacagt ttgatattgt agagccagga atccatccca 720  
 gggmagtggg ccagaaggta gtggctgact gccatgcccg aggacgtccc caggagctgc 780  
 cgtgaa 786

<210> 59  
 <211> 837  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> misc\_feature

&lt;222&gt; (1)..(837)

&lt;223&gt; n is a, g, c, or t

&lt;400&gt; 59

```

tctggnnccc cgggacgtnn ttgggagctg ccctgagctc ccacctgctg ctgccagtac      60
tagcacaggg tcctcaagtg atggctgctg gtgaattatt tagaatctcc atgggcaggg      120
cattctgctt tttagcactg tgtcttgacc tgttccaaga ccattctcca aggagagcca      180
gcagctggtg ttgtaagttc ttcccatgac aaataagccc aagacctcac ttaggaaaca      240
tacaatgatt atatgatctt gggagtcagc cctagaaggg cccttcttct cttgcttcaa      300
gctaaaaaga ctctggacaa caaaagaggg agtggtgct aagtaacttg caactaccac      360
ttcagctctca ctgcagctgc aaagatagga acagagaagt tttagggtgag aaactccttt      420
ttccaagaa actgtgatga accagtgtta cagtttaggg agagagctct gtagacaagg      480
agggacctaa ggacccccag gactcaccac cccacacct agctccctg gtcacctggt      540
acgtaagcag gtaggctctg cttagcatag tgctaagatc acatcttgct cagagtgtac      600
aaactcagga aagctggcat taggtagtat cacaagtga aaaatacctc aaccagtggc      660
cattggaagt gcggaagtac atgccatact cactgcaagg ttctccattc cagctgccgt      720
actgtgtaat acgacttaat atcttcagag natcaagggt aatttcaaat ttgtgtcttc      780
aaagaacatt tctttttnnt tcttttgggg ncagtactgc gcacatttta actagga      837

```

&lt;211&gt; 866

&lt;212&gt; DNA

&lt;213&gt; Canis familiaris

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(866)

&lt;223&gt; n is a, g, c, or t

&lt;400&gt; 60

```

ttgtcgagcg gataacaatt tcacacagna attccagcac catgcactct ctgagacagg      60
tgaggatttt gcagcagctg ataaggacac aagtgaacag gagcataata atgaaaacac      120
aaagactagt tagctgttac tacttgcttc tagggcttct agtgttctct gttgtgatac      180
ttggtcaaat gttgtttggg agtcactgaa gaatgcttca tcatttgcaa agataggacc      240
ctaacttgta agccccctaa attaaaagaa tgcttttttag tacaaaatta atgatcttag      300
tcacaaaaag caaagaagaa atcaaaatca caaagtcac attcaaagtt gtattcttta      360
tagcaaaaat ggggcaagct acaggattgc caaaagtctt ataaaacagg aggaaggttt      420
atgaaatgat gctcagagag aatgcagaat gtgctattag cacaaatcct ttctgaaatg      480
gaacctgagc aaagtgatgg catttgatgt agaggaatag ccaccatcac atatgtgtga      540

```

gagaaaatag tttgctttgg ggatgaacaa taccaccggt gtacaaagca tgaataagca 600  
 ctgggaaaat gtatagtatg tataacagag ggacttttat ctgtttgga ttgaaaatca 660  
 atgccattaa aagtaggaac aattgggtat tgggnctgat tttttaaag aattcattta 720  
 tttnttttng gggganagaa nneccccccc cctntnacc cnggggaaan annnaggggn 780  
 aaaaaanaat nttnagccna ctnttttctt nntgggnccc cgggnggggg ctttancnca 840  
 aanccngna aannannntn ngncn 866

<210> 61  
 <211> 886  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> misc\_feature  
 <222> (1)..(886)  
 <223> n is a, g, c, or t

<400> 61  
 ttgngaaccc gcttgccaaa cctacaggtg gggcctttca agaacataag cccaaataag 60  
 cactggcaca tagtaggagc agcataaacg ctccccctcc tattcctaac ccaccaagaa 120  
 ttctagattg acagtttttt ctttgagtat tttaaagatg ctgcttcctt gacttcttgt 180  
 ttgcaaattt ctgatgagaa atctgctgtc attttatctt ccttcctttg cataatgatg 240  
 tatctttttc tctctgcttt taagattttc attttatcac tggttctaag caatttaatt 300  
 atgatgttcc ttggtatagt gctcttcata tttctattag gagtttggtg agcttcttgg 360  
 atttgtgagt ttatagtttt tatcaaattt ggcaagtttt cagctactat ttcttcaact 420  
 ttttttttcc tgtcctcctt tgactcctcc tcattcccat atttctcttg tccttcaggg 480  
 actecagtta tctgtatggt aagctcattg ataccctatt tgtgtatatt ttaaggcttt 540  
 ttattccttg tatttcattt tggatagttt ctactgcaat gttttcaggt tctttaacct 600  
 cttttttttt ttccccocag taatgtctaa tctgctcttc atcccaaaga catgtagtgg 660  
 tgtgtgtgct aaaaatccca gacaatgttt ttatgattcc taggtatttg ctttggggct 720  
 tttcaaagat ttccatatt tctacttctt tggccatata gaatgcggn tttattattt 780  
 tttagnggcc tatgctacta aatcctataa ttntgggac tcnnttgatt nagnntnnc 840  
 tttttattta ttnattaagn anggttttat tgggagtng attncc 886

<210> 62  
 <211> 728  
 <212> DNA  
 <213> Canis familiaris



&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(728)

&lt;223&gt; n is a, g, c, or t

&lt;400&gt; 62

```

ggattgtcag cggataacaa ttccacacag aattcccagg acccagcatg atgcctgggtg      60
tgcacatggg tgggccctcc tatgtaagcg tcaccactcg ggagcagtg cggggatgcc      120
tggatgcgcc ggctcctgcg ttaggggtgc tatcaggaca ttgctgggtt gccacctctg      180
tctgaggctc cagagagcga ggggacaccc cacatcatga atgcctgtg gggttaccag      240
tgggggcaat tacctgcatt gctcctgggc ctccagcgcc tcatctgtga aatgggtaca      300
ttcatatcac gtatgggaga gggctgccgt ggggtttaat ggaggcaacc catttgagcg      360
ctggggcccg caccgtcct gctcttactg tgactatggc cagcgtcact gttgcagggc      420
cttgaccggc cggggtggac gctggtgcca ccgttgctct ctcccagggg gggaggagac      480
aggcctgcgg ggcggactca ccgtggcggt gacggtgagc tggtaggcct gcgtgggtctc      540
gtagtccagc tcgcggaacca ccgtgacgat gccgcggggc ctgtcgatgg cgaacaacgg      600
ggaccggggc tggaaggagt acaggacgct gcccctgca ccaagtcggg gtcogtggcg      660
ttacgataaa atgggtgtcc ccaccggcgt gttctggggg ccaagcaaac aaccaaggtg      720
agtgggct                                         728

```

&lt;210&gt; 63

&lt;211&gt; 785

&lt;212&gt; DNA

&lt;213&gt; Canis familiaris

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(785)

&lt;223&gt; n is a, g, c, or t

&lt;400&gt; 63

```

attgtcgagc ggataacaat ttccacacaga attcctaaaa cccttactgt tgtttttata      60
tggcacttcc tgatgtgatt gcaggctttt agcaaagcca tttttgttaa caaaaaatga      120
tttaaattct tttaaacaag tgtttagtga caagtcagta ttagtcatc tagttattga      180
tacagcacc ataaaattta tctctgaggg gagggatcag gaggaatgt gggcattcta      240
acttaatgat taataatatg tgtctataac aaatgtgatg gctaagttat aaaatattta      300
aaaaattttt tcttgaggt atttataaca gcaatgatgt agcagtatca ttocaaatg      360
tggatatctg ctcaggatct agcactcctg tctccagttc tcatttaoct cagcagctct      420
ctgggcattt gcaacaagtg ggagcactct cccatcagc agcatcatct gcaaccctg      480

```

```

ctgttgctac aactcaggtat atcattacag tgcctatgaag taacctgtag atggctttgt 540
cgtttttgaa agtgagtttg attggagaag aaagaaacct tgcctatagaaa ccttcctata 600
taaattccta taggaattta taagtatctc catttggtttt gacacgttag tggatataat 660
agacattttt atgtgatatt catgagaaag gacaaaagaa tacattggca ttaactgatt 720
cttttcagtt tctgagtttc taatttttcc tgaagatgna aacaaaaatt tggggggaac 780
tttta 785

```

```

<210> 64
<211> 981
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(981)
<223> n is a, g, c, or t

```

```

<400> 64
ttggnaancg tcagaccaag ttactcata tggatccaa agtgcttgag actgcatttt 60
tttcaaattt tgcaatattt gcattataat caccagttaa gcatccgtaa tccaaaaatc 120
ctaaacctac aatgctctaa taaatatttc ctttggctgt gttgggtgcaa aaaatgtttt 180
ggattttgga agacttcaaa tttcacatta gggataccct gaggggaaaa aatagttttt 240
gtttttaaga ttctttcact caacaacaat caacaaggta gacttctgtg atcaaatgtg 300
tgaggatttc tccccaccaa taagcaatca attctgcagc agacaccaag tgggtatcct 360
ccaattcaag tctgacatta cctacctgga gaaagcgtca gatctcacag gttgatggct 420
cagtcacaca agactgctcc ctacttctga tgcatacac aagccacagt ttgttttacc 480
tgtgcttcta actgactgga tataaactgg gaatctcatg agccctctt tgggttcggt 540
taatttgcta gagggttca cagaactcag ggaatcacat ttattagttt attataaagg 600
atatacagtt gaagagatac acatggcaag gtatgccctc cctgggaaca ccaactctcca 660
ggaacctnct tttgttcttg tccagaagct ctctgaatcc tctctcttg ggccttttat 720
ggagacttna ttagatgggc atgactgaca cacatgtaga aatgtgactg gagaaaaaat 780
atatgatcta atattaatag actggggaaa ctcanaggg cctgtntgtt caaatnttc 840
nggmcntttt gggtagcatt nctnctcca gggtnnggg gngnacnttt ttgaaagaaa 900
gtntttgacc ctanncaaaa gngggggaag annaantnct cttnnggcag nnaaaaaaaaa 960
aaaaattttt ttttnggnt n 981

```

<210> 65  
 <211> 981  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(981)  
 <223> n is a, g, c, or t

<400> 65  
 ttgnaancg tcagaccaag ttactcata tcggatccaa agtgcttgag actgcatttt 60  
 tttcaaattt tgcaatattt gcattataat caccagttaa gcatccgtaa tccaaaaatc 120  
 ctaaacctac aatgctctaa taaatatttc ctttggtgtg gttggtgcaa aaaatgtttt 180  
 ggattttgga agacttcaaa tttcacatta gggataccct gagtggaaaa aatagttttt 240  
 gtttttaaga ttctttcact caacaacaat caacaaggta gacttctgtg atcaaatgtg 300  
 tgaggatttc tccocacca taagcaatca attctgcagc agacaccaag tgggtatcct 360  
 ccaattcaag tctgacatta cctacctgga gaaagcgtca gatctcacag gttgatggct 420  
 cagtcccaca agactgctcc ctacttctga tgtcaatcac aagccacagt ttgttttacc 480  
 tgtgcttcta actgactgga tataaactgg gaatctcatg agccctctt tgggttcggt 540  
 taatttgcta gagtggctca cagaactcag ggaatcacat ttattagttt attataaagg 600  
 atatacagtt gaagagatac acatggcaag gtatgcctc cctgggaaca ccactctcca 660  
 ggaacctnct ttgttcttg tccagaagct cttcgaatcc tctctcttg ggccttttat 720  
 ggagacttna ttagatgggc atgactgaca cacatgtaga aatgtgactg gagaaaaaat 780  
 atatgatcta atattaatag actggggaaa ctcanaggg cctgtntgtt caaatnttc 840  
 nggncntttt gggtagcatt nctnctcca gggtnnggg gngnacnttt ttgaaagaaa 900  
 gnttttgacc ctanncaaaa gngggggaag annaantnct ctttnggcag nnaaaaaaaaa 960  
 aaaaattttt ttttnggnt n 981

<210> 66  
 <211> 1005  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(1005)  
 <223> n is a, g, c, or t

<400> 66  
 cttagctngc ttgccaaacc tacagggtggg gtctttcaaa aaacagacat gcagacttta 60

```

acagataata aggtttttga ggttttcoogt ttatgtatatt actcgagaaa gcaagagctt 120
tatttatatta tttttgagac ggagtttcgc tctgtcgecc gggctggagt gcaatggctc 180
catctcgtct cactgaaacc tctgectccc gggttcaagc gattctccca tctcaacctc 240
ccgagtagct gggattacag gcgcgcgacg ccacgcctgt ataaaaatac taaaaatgca 300
aaaataattt ttgtatattt agtagagatg gcgtttcatc atgttggcga aactccaggc 360
tggtctcgaa ccttgacctc ggtgatctgc ccgcctcggc ctcccaaagt gctgggatta 420
caggcgtgag ccaocgcgac cggccaagag ctttataaag atggaaaacg aagcagaactt 480
tctgccaag ccatgctttt ggataaggat tacactactt tgaaatctta catatatagc 540
acttgccaa ctatcaaaac tgcacaaaacc ttcactaatt gcaattattc cctttaacat 600
ctcgagttac ccaatccgc aaaaaacaag tttagtgcc accaggtaat aatacatcca 660
ggaaaaataat tccaagaaca gacgtttaag aactacagag aaaaacatac tttttctac 720
aagaaaaaat cttagaggac agtaccaggg nccttatctc tgtagcatg atttatattt 780
cacgtaacgt tggcccagtc actgctncat tntaaancna tagccanggc anatagaaag 840
tctgaacana ttgacngcna ngggtttaaa ttttttacca ggnaacaaan cctggcaaac 900
tgccancang ggtgccc aaa tgctggncn gggccctgg aagnaaacgg agggctttga 960
attttttcc nttnngaac ngmncngnt ttnggcnaaa tnttc 1005

```

```

<210> 67
<211> 863
<212> DNA
<213> Cercopithecus aethiops

```

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<220>
<221> misc_feature
<222> (1)..(863)
<223> n is a, g, c, or t

```

```

<400> 67
nttttggng nntanctnt ananatnngc caattattgg ggggnacctt catcataagt 60
attaatataa taataataat aagtaatagt aactagtaac aacaataaaa aggaaatcag 120
cggaaagtca ggaaaaatgt taaaaaaaaa ttggaataac ttactgtagc tgaagatcaa 180
aaaaatctca ctgtaaaaaa acaaaaaataa aaatagccca gattagaaaa acgggaggtg 240
caaaaatgtc aagtcagtaa agttcatttc ttttctctt ccaaaagcag tttccacaaa 300
aaccgcaagg ataaagtatt cagtagcaga caagcaaagc cctttcgaca tcatcaatca 360
atcttaaaaa tacacgagga agtagagagg tcagtttatg agaggctaaa aggtcctcc 420
tcctctaacc caactgctgc agaaaaaata gaaatagaaa ttttaaaaat tacatcttaa 480

```

atccaggtcc cggttttgga aacaattaaa aaaaaaacac ctgtacattt gccgtagtgc 540  
 acaccaagtt gcatcattat gtttaaaatg tctttataaa atcagttttg gaatggaatg 600  
 tgtgtgttct ggaaggggtgg ggaagggagg ttaaaaatca aagctgagct ccagtgagta 660  
 gggatgggggt tcgccttgct gcctgtgaa agggaaagga cagatnagtc aanttnctaa 720  
 aaatgtntgc cctaانccn anaaaaaact ttgnntttng aantaaaaat ttggtaagct 780  
 ttaaattccc tggnggggaa nccنntaaa nacctttنca ngnnngntta aaattttaan 840  
 aaaangggnn naaaaaaaa ncc 863

<210> 68  
 <211> 918  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(918)  
 <223> n is a, g, c, or t

<400> 68  
 cnnnttctgg nngatnaaan tnnttnnnna nttنccaat nnattggggg gaannnttca 60  
 tcataagtat tnatataata ataataataa gtaatagtaa ctagtaacaa caataaaaag 120  
 gaaatcagcg gaaagtcagg aaaaatgtta aaaaaaatt ggaataactt actgtagctg 180  
 aagatcaaaa aaatctcact gtaaaaaaac aaaaataaaa atagcccaga ttagaaaaac 240  
 gggaggtgca aaaatgtcaa gtcagtaaag ttcatttctt ttctctttcc aaaagcagtt 300  
 tccacaaaaa ccgcaaggat aaagttttca gtagcagaca agcaaagccc ttctgacatc 360  
 atcaatcaat cttaaaaaata cacgaggaag tagagaggtc agtttatgag aggctaaaag 420  
 gtcctcctc ctctaacca actgctgcag aaaaaataga aatagaaatt ttaaaaaatta 480  
 catcttaaat ccaggtcccg gttttggaaa caattaaaaa aaaaacacct gtacatttgc 540  
 cgtagtgcac accaagttgc atcattatgt ttaaaatgtc tttataaaat cagttttgga 600  
 atggaatgtg tgtgttctgg aaggggtggg aagggagggt aaaaatcaaa gctgagctcc 660  
 agtgagtagg gatgggggtc gccttgctgc cctgtgaaag gagaaggac agattgagtc 720  
 agagtctctc aaaaatgttg tgcctaaac cccaagaca gaaacatctt gtttatntn 780  
 gctaacacaa tntttntgna naatnatnaa cctcccngg ggagggnacn ccctnnnnaa 840  
 aannnccctt nccanggant gnnttnaaan ttttnaana tnantggggg nanaaaaatna 900  
 acnaانccct gnnaattn 918

<210> 69

&lt;211&gt; 887

&lt;212&gt; DNA

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(887)

&lt;223&gt; n is a, g, c, or t

&lt;400&gt; 69

```

tncantcttt nnnnggcna nacgcgcgc nantcgccaa tnactggggg ggnancttca      60
tcataagtat taatataata ataataataa gtaatagtaa ctagtaacaa caataaaaag      120
gaaatcagcg gaaagtcagg aaaaatgtta aaaaaaatt ggaataactt actgtagctg      180
aagatcaaaa aaatctcact gtaaaaaaac aaaaataaaa atagcccaga ttagaaaaac      240
gggaggtgca aaaatgtcaa gtcagtaaag ttcatttctt ttctctttcc aaaagdagtt      300
tccacaaaaa ccgcaaggat aaagttttca gtagcagaca agcaaagccc ttctgcacatc      360
atcaatcaat cttaaaaata cacgaggaag tagagaggtc agtttatgag aggctaaaag      420
gctcctctc ctctaacca actgctgcag aaaaaataga aatagaaatt ttaaaaatta      480
catcttaaat ccaggtoccg gttttggaaa caattaaaaa aaaaacacct gtacatttgc      540
cgtagtgcac accaagttgc atcattatgt ttaaaatgtc ttataaaaat cagttttgga      600
atggaatgtg tgtgttctgg aagggtgggg aaggaggtt aaaaatcaaa gctgagctcc      660
agtgagtagg gatgggggtc gccttgctgc cctgtgaaag gagaaggac agattgagtc      720
agagttctc agaaatgttg tgcctaacc cccaagacag aaacatctgt ctttcagct      780
aacacatttt ggnaagcatn acatncactg ggatggacag ccncntaaaa aacctnnn      840
ngncnnnttt naanttttaa nnnaaagggg nnnaaataa naaccn                      887

```

&lt;210&gt; 70

&lt;211&gt; 897

&lt;212&gt; DNA

&lt;213&gt; Cercopithecus aethiops

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(897)

&lt;223&gt; n is a, g, c, or t

&lt;400&gt; 70

```

ctttggggng tnntcanac ntttancac nntnntcgcc antcnccttg aggggnaaac      60
ctatgcctt ctatcgnctt cttgacgagt tcttctgagc gggactctgg ggttcgaaat      120
gagctagccc ttaagtaacg ccattttgca aggcattgaa aaatacataa ctgagaatag      180
aaaagttcag atcgaggtca ggaacagatg gaacaggggc gaccggtcga ccggctcgacc      240

```

ctagagaacc atcagatggt tccaggggtgc cccaaggacc tgaaatgacc ctgtgcctta 300  
 ttgtaactaa ccaatcagtt cgcttctcgc ttctgttcgc gcgcttctgc tccccgagct 360  
 caataaaaga gccacaaacc cctcactcgg ggcgccagtc ctccgattga ctgagtcgcc 420  
 cgggtacccg tgtatccaat aaacocctctt gcagttgcat ccgacttggt gtctcgctgt 480  
 tccttgggag ggtctcctct gagtgattga ctaccggtca gcgggggtct ttcaatgatg 540  
 gtgatgatga tgatgataat gacactgatg atttttaacc ggattaaaat cgagtttttc 600  
 tgaatgtttc taagaatttc tccggectcc tgattgactt tggagttttg catcttgga 660  
 gagaaagcga aggcattagt atttttaagt ggattgatca cataaacctt ttctctccca 720  
 accccaccct tgccttcttc cccttcccca cactgaacag aattttactg gctgntaagt 780  
 ctatgacctt attttttctt gatctttaac ttaactgntt tagagcatct ntggacgncn 840  
 ggattttnaa attttttnat tttnggnttt ttnntttnaa annttnnatt gggaaan 897

<210> 71  
 <211> 878  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(878)  
 <223> n is a, g, c, or t

<400> 71  
 tcggggngnn ctccactnnt gntgcnnntc nncgccantc cncttgnggg gnaaaccatc 60  
 gccttctatc gncttcttga cgagttcttc tgagcgggac tctgggggtc gaaatgagct 120  
 agcccttaag taacgccatt ttgcaaggca tggaaaaata cataactgag aatagaaaag 180  
 ttcagatcga ggtcaggaac agatggaaca ggtcgcaccg gtcgaccggt cgaccctaga 240  
 gaaccatcag atgtttccag ggtgccccaa ggacctgaaa tgacctgtg ccttatttga 300  
 actaaccaat cagttcgctt ctcgcttctg ttcgcgcgct tctgctcccc gagctcaata 360  
 aaagagccca caaccctca ctcggggggc tagtcctccg attgactgag tcgcccggt 420  
 acccgtgtat ccaataaacc ctcttgcaagt tgcattcgac ttgtggtctc gctgttcctt 480  
 gggaggggtct cctctgagtg attgactacc cgtcagcggg ggtctttcaa tgatgggtgat 540  
 gatgatgatg ataatgacac tgatgatgtt taaccggatt aaaatcgagt ttttctgaat 600  
 gtttctaaga atttctccgg cctcctgatt gactttggag ttttgcattt tgggagagaa 660  
 agcgaaggca ttagtatgtt taagtggatt gatcacataa aocctttctt tnccaaacccc 720  
 acccttgccc ttatccctt cccacactg aacagaattt tactggctgn taagtctatg 780

accttatttt tctgatctt taactnactg ntttagannt ctctggaogn cggnntttna 840  
 aatttnttat tttgggtttt tantttaaan ctnnattn 878

<210> 72  
 <211> 964  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(964)  
 <223> n is a, g, c, or t

<400> 72  
 cttctggggn gannnaanca nttcgnnan nntccncca atctacttgn ggggcaaacc 60  
 catcgcttc tctgttctt ctgacgagt tcttctgagc gggactctgg ggttcgaaat 120  
 gagctagccc ttaagtaacg ccattttgca aggcattgga aaatacataa ctgagaatag 180  
 aaaagttcag atcgaggta ggaacagatg gaacagggc gaccggtcga cgggtcgacc 240  
 ctagagaacc atcagatgtt tccaggggtc cccaaggacc tgaaatgacc ctgtgcctta 300  
 tttgaactaa ccaatcagtt cgcttctgc ttctgttcgc gcgcttctgc tccccgagct 360  
 caataaaaga gccacaacc cctcactcgg ggcgccagtc ctccgattga ctgagtcgcc 420  
 cgggtacctg tctatccaat aaaccctctt gcagttgcat ccgacttctg gtctcgctgt 480  
 tcttggggag ggtctctctt gaggatga ctaccgtca gcgggggtct ttcaatgatg 540  
 gtgatgatga tgatgataat gacactgatg atttttaacc ggattaaaat cgagtttttc 600  
 tgaatgtttc taagaatttc tccggcctcc tgattgactt tggagttttg catcttggga 660  
 gagaaagcga aggcattagt atttttaagt ggattgatca cataaacctt ttttttcca 720  
 accccacct tgncttatn ccttnccca cactgaacag aaantactg gctggnannn 780  
 natgancta nttttnnng ncttnaanta acnggnnnna anaaanng gcnnccggnn 840  
 nnnaaaaan ttnnnnnng nngntttttt naaaaancnt nnttnnaaaa ntaaaancgg 900  
 nnnnnaaaa nggggggggn cncnnannn tnannnnngg ngggttttcc nnaaancntt 960  
 ttcc 964

<210> 73  
 <211> 986  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(986)



<223> n is a, g, c, or t

<400> 73

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catccttctg nnnngnaana aacgtncnnn nnnncnctcc cnaatttaac ttgggggggn      60
aaaancatcg ccttctatct ttcttcttga cgagttcttc tgagcgggac tctgggggtc      120
gaaatgagct agoccttaag taacgccatt ttgcaaggca tggaaaaata cataactgag      180
aatagaaaag ttcagatcga ggtcaggaac agatggaaca gggtcgaacc gtcgaccggg      240
cgaccctaga gaacocatcag atgtttccag ggtgccccaa ggacctgaaa tgaccctgtg      300
ccttatttga actaaccaat cagttcgctt ctgcgttctg ttgcgcgcgt tctgctcccc      360
gagctcaata aaagagocca caacccctca ctcggggcgc cagtctcccg attgactgag      420
tcgcccgggt acccgtgtat ccaataaacc ctcttcagct tgcacccgac ttgtgggtct      480
gctgttcctt gggaggggtct cctctgagtg attgactacc cgtcagcggg ggtctttcaa      540
tgatgggtgat gatgatgatg ataatgacac tgatgatttt taaccggatt aaaatcgagt      600
ttttctgaat gtttctaaga atttctccgg cctoctgatt gactttggag ttttgcattct      660
tgaggagaaa agcgaaggca ttagtatctt taagtggatt gatcacataa accttttctc      720
tcccaacccc acccttgccc ttatccctt cccacactg aacagaattt tactggctgt      780
taagtctatg accttatctt tctgatctt taacttaact gntttanagc atctntggac      840
gnnngnatct naaanntttt tatctnggnt tttnatctta aannttnatt ngnaaanntt      900
naactgggct gnanaaaagg gnggggncta ctnaaantnn nnacggggagg gntttncctg      960
nanncanttn ctccnnttcc ntgaan      986

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<210> 74

<211> 748

<212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc\_feature

<222> (1)..(748)

<223> n is a, g, c, or t

<400> 74

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ttttttgcnt taaccgtatcg ccgctnnega ttgcagcgc atcgcttct atcgcttct      60
tgacgagttc ttctgagcgg gactctgggg ttcgaaatga gctagccctt aagtaacgcc      120
atcttgcaag gcatggaaaa atacataact gagaatagaa aagttcagat cgaggtcagg      180
aacagatgga acagggtcga ccggtcgacc ggtcgacct agagaaecat cagatgtttc      240
caggggtccc caaggacctg aaatgacctt gtgccttatt tgaactaacc aatcagttcg      300
cttctcgctt ctgttcgcgc gcttctgctc ccgagctca ataaaagagc ccacaacccc      360

```

accctcttgc agttgcatcc gacttgtggt ctgctgttc ctggggaggg tctcctctga 480  
 gtgattgact acccgtcagc gggggtcttt caatgatggt gatgatgatg atgataatga 540  
 cactgatgat ttttaaccgg attaaaatcg agtttttctg aatgtttcta agaatttctc 600  
 cggcctcctg attgactttg gagttttgca tcttgggaga gaaagcgaag gcattagtat 660  
 ttttaagtgg attgatcaca taaacctttt tntcttccaa cccacacctt gcccttatnc 720  
 octtccccac actgaacaga attttact 748

<210> 75  
 <211> 881  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(881)  
 <223> n is a, g, c, or t

<400> 75  
 tntcttgagg acccgatcg ccgcttccga ttgcagcgc atcgcttct atcgcttct 60  
  
 attttgcaag gcatggaaaa atacataact gagaatagaa aagttcagat cgaggtcagg 180  
 aacagatgga acagggtcga ccgggtcgacc ggtcgacct agagaacct cagatgttct 240  
 cagggtgccc caaggacctg aaatgacct gtgccttatt tgaactaacc aatcagttcg 300  
 cttctcgctt ctgttcgagc gcttctgctc cccgagctca ataaaagagc ccacaacccc 360  
 tcaactgggg cgccagtcct ccgattgact gagtcgccc ggtaacctgt tatccaataa 420  
 accctcttgc agttgcatcc gacttgtggt ctgctgttc ctggggaggg tctcctctga 480  
 gtgattgact acccgtcagc gggggtcttt caatgatggt gatgatgatg atgataatga 540  
 cactgatgat ttttaaccgg attaaaatcg agtttttctg aatgtttcta agaatttctc 600  
 cggcctcctg attgactttg gagttttgca tcttgggaga gaaagcgaan gccttantat 660  
 tttttagnng gtnggnnaca tataaccttt ttttttccaa nccccccctt ncccttttnc 720  
 ccttttcccc actgaaaaaa attttaacng ctgnnaannn tnnnacctn ttttncnnn 780  
 ncttnannna annggttnaa gaccnnnnng ggcnnnngn ttnnaaant ttttntttng 840  
 ggnttttnt ttnnaancnnn cnttggnaaa ntttnaanng g 881

<210> 76  
 <211> 906  
 <212> DNA  
 <213> Cercopithecus aethiops

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(906)

&lt;223&gt; n is a, g, c, or t

&lt;400&gt; 76

```

cannnttctg gggngtnnnn aactnannnn nnnnatcgcn nccacantnn nnttgggggg      60
aaaaacctga atacatttgt ngttatttcc cttagatctt tttttttttt tttttttttt      120
ttgagacatc tcaactctgtc acccaggcta gagtgaagtg gcacaatctc tggctcactg      180
caaccccccac ctgcctgggt caagcgattc tcctgcctca gcttcccagag tagctggtac      240
tatagggtgtg caaccaccaca cctggctaata ttttttaaaa aatattttta gtggagatgg      300
ggtttcacca tgttgaccag gctggctctca aactcctgac ctcaaaggat ccacctgctt      360
tggcctccca aagtgtctggg attataagca tgagccacca tgcagcctg tttcttttag      420
atcttgattt gatattctgg atatgaatga aagaaaatta atgagtgttt caaagtctaa      480
ataaggaagc tccacagata atattaacat ttctctgac tagtcatatt tattattgtg      540
tttcaattag aagtggctgt aggctctgaa agacacacta taaataaagc ctccccctca      600
tacacctca ctcaacca cacttacacc aatgcaattt ttagacagaa acacaagcaa      660
gaaataggat agattttttt taaaaaatgg gcattgggta aattttctgg tcatattaaa      720
aaanntnttt nagaactccc aanggggggc cattaataga gacctnattc actgnnggaa      780
nnaaannggn aaattncnan aattnctnac aatntttagg ganttgangn aaaatnttnn      840
gtnnntgnaa ctttctagn ggncnnnttn ngccctatnc ccaggntttt tatnctaaac      900
cccntc                                          906

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&lt;210&gt; 77

&lt;211&gt; 909

&lt;212&gt; DNA

&lt;213&gt; Cercopithecus aethiops

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(909)

&lt;223&gt; n is a, g, c, or t

&lt;400&gt; 77

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cntcttnngg gngttnaanc tgnctnnnaa tgcntcacat tnattnnggg gaaaaccgta      60
ctgacttatt atgagaggtt ttgtctcttg ttaggatcca gtaggttga ggtgcaacta      120
ttctctact ttactcttcc acctccaga gaactctgcc aagaaccatg ttaagactgc      180
ttctgtcttt aactactaat agtcttgatt ataggaacgg aattctgtga tcaagtaggt      240

```

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tctaagaact taacataaaa actggtatt aatgcatttg caaaatttgc attttaaatc 300
caaggcaaga acaggtcagg caaaaatgga atccaaacac caaattgtta aaagttbtaa 360
gtccatttct cttgttagtt tgcaacttaa attactaatt ctctaattgt ttagagcaga 420
agttggtaaa ttgtttctgt aaaaaaattg tttctttaaa ttgtttcata atcaaaattt 480
taggttgtgt aggtgatact gtttctgttg aaattattta atctaataaa atggacatag 540
ctgtgttcta acaaaacttt atgattaacc tgacaggcca gatttgaaat gttagcaggt 600
ttgcacaccc ctactttaga aaaactcagt ctttatagct tccagttaca agatgtatct 660
tttttttttt tttttttaaa taagacagta ttatttcaaa tgcgggtgg ctcataccna 720
aatttgtttc cccnttcttn antttttnaa angtggggcc caaanacttn aaaaggtngn 780
anncnttttn nntaanaaaa nanccattta ggggnnttn caacccctnn aaaaantttt 840
ttcttnaaa aanqantnca naaaannntn ctnaaaaaan naaaggggcc caccnttnt 900
ttttaaaac 909

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<210> 78
<211> 890
<212> DNA
<213> Cercopithecus aethiops

```

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<220>
<221> misc_feature
<222> (1)..(890)
<223> n is a, g, c, or t

```

```

<400> 78
gnntnncnnc tttnnngat cagccgcnc ncagnncccc accaatccna cttggtgtaa 60
accccccagc agggctcttg gctttcttct tgcttctcca aaatgggcct ggcttccag 120
gagacagccg agagcgctc gccctgtctg gaagggcagc ctgggagctg gagttggcaa 180
acgggagggg acgggaggag gcccagggga gggggcgctt tcccttagct ttcagcgaca 240
tctgctggcc gtgcgctgaa ctgccgtac cccagaggcc agctggagac caattttgag 300
ttgtgagcag ggaaagagag gaggggttcc aggacaatca ggtctggagc ttcagaaac 360
attccaaaaa cacagtttag gctttttaat tgttcactra gtcattctcc cgggggtctag 420
ggagaaatcg gactcagact cggatctttg gggacctacc gcagcatgat aaccaggtg 480
tacctggggc tcatgggggc ctggggatca gggaggcccc tcacctgcat tcaactgtgtg 540
ccaagcactg gcctacatca ctgacatttg ctgtctcgct gcgggtgctg tgatcttgct 600
gctgtgctca ttgacagat gaaaacgctc aggttgtgag agaaccocaa agccagagga 660
ttcccttgat cactccctt ccttcatgcc catagtcatt cctcttcaa agcctatccg 720

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tcccacctcc aaagcacacc atggatgcc atccttggcc catcatcgtt accctctnag 780  
 tgccagcctg cctganccccc tcanttnaag tcccgcctcc tggccttttg cagaagcatc 840  
 ccaccagaat ctncagcca cccctccna nttntntntt cccaaatggc 890

<210> 79  
 <211> 965  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(965)  
 <223> n is a, g, c, or t

<400> 79  
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 agccccaagg tggccattgt cagggagggtg cttgctatgc agatgtgocg ttcaaaggca 120  
 tgcagatatg aaagcatcgc tccctcagggt gggagacaat gggaagggtcg agagcactgt 180  
 ggtaggagc aaggcttttg aattagcagt cctgcattc aaatcctagc ttacttgcc 240  
 tcatgacagc cgtctgtcct tgagcaaat tgtttaacct ctctggacct gtctatatct 300  
 gtaaaaaggg ccaacatggt gtacccaaa gccttgctgt ggtgatctca ttaagatatt 360  
 tcatgtgaat atgtgtgag tggcctcacg taggagggtgc ttactgactt ctcccaagcc 420  
 ccctcctctt catcgtact gccgtctgc gtatcctcca gcctcctccc acgctttctc 480  
 tctctgact ttttgggggt gagggaggcc atttctgagt cacttgctcc tggacttgat 540  
 gaattccatt cgtgtggcgg gggcagcagg gccagtgtg aaccagcagc tccccaacc 600  
 tgcccaactat accactcaag tgagtccaag ctgtgatgcc cctggctgcc tccccactt 660  
 cccttgagcg agctgggagg acaaagattg gactctgagg atcagcctga gacttaagat 720  
 ggaggctgtg ttcccgagag ccaggggtgg gcatgccagg aagcactctg gctccacgga 780  
 atgtgcaact gccccggggc tggcanacca nacttcctt gnttntctgg gtctnacagn 840  
 cncancctgg cctgggctgt ttttgcntgn tgnacctgcc tnaaannggn aaancctggn 900  
 ancctggagn cttecnaggt ttngnttttc caancncca aaattangnc naaccngnct 960  
 nnggc 965

<210> 80  
 <211> 891  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>

<221> misc\_feature  
 <222> (1)..(891)  
 <223> n is a, g, c, or t

<400> 80  
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 aggtgaggggt gtccagagat gtcttgcaaa tggcaatgtc ccaggocatg gaaacaggaa 120  
 tatgggctca aatccattta tggccaggca tgggtggctca tgccctgtaat cccaacactt 180  
 tgggaggtca aggcaggagg attgcttaag ccaggaggtt caagaecgtc tgggcaacgg 240  
 agaggagacc ctgtctctac aaataattaa aaaattatct gagcatagtg gcacatgcgt 300  
 gtgggtccag ctactcggga ggctgaagtg ggaggatcgc ttgaggccaa gaggtcaagg 360  
 ctgcagtga aatgtgatcat accacggcac ttgagcctgg gcgacagagc aagaccctgt 420  
 ctttcttttt ttttttcaaa aaaaaaaaaat ccatttataa ttaacatgg ggcctcacg 480  
 ggaaagagtt ctgtcttgtg tgagtgggtcc agtgttttgg atgggctgga actttgcact 540  
 tgatgtgttg taattcattt tctagagtct atgtcgtgaa ggtccttggg gtgatagagc 600  
 cttggaaaaa tgttgtttcc ctgtggatta tctaaactag atccaagaac atgaaagacc 660  
 atccctcagg gagctggcat ttgtctaaaa accancattn cctgggccat ttgattgggg 720  
 ntcttgcctc actgcaaang ggggacttgc aaaattttac tnatgnccn nttgtnttt 780  
 ttntccaagg ggnntttana aaatttttct tnnnntttt ncnnaanacc ccnttnnant 840  
 tntnttttnc nccccnttt ntntaacna nggggggntt ttnaacnncc n 891

<210> 81  
 <211> 803  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(803)  
 <223> n is a, g, c, or t

<400> 81  
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 caactctctc ttccacctg cccccaaaac tccctccac ctccctccac atgtatcctc 120  
 ccacttcctt ccactcatgt aatgagaggt gctgatgagt cacaggagag gtagccctag 180  
 ataaccaaca gactgcaaaa cggacagbcc ctggatgtct gagccagtgt ttgtgcactg 240  
 cattgactgg ctctcgtag ttttttctctg tagttgctaa agcctgtaag gtctgtgtga 300  
 tgaatatattt ctaacacatc ttagaagaac ataatgcaag acagaatgaa aaactagaga 360  
 ggcagaaacc cccaaagtaa gtagtgggaa attaccaggt atataatagg tcaagcctgc 420

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tctgcaggag ctcaagggat ttagcattc ttatcecaaa ccactgaatc ctgggcaaaa      480
ataagaagtc gectaatttt agtattacca gcttcccaac ccggggcatt cttcatotta      540
ctcaagctgt ccagaggccc cagggtgact ccctataagt cccatgggtg gctgagatct      600
atttagaggc acaagggtat ctccttataa gtcccatggg tggctgagat ctatgagaag      660
catcttgggg agagtgoctc tggccaccag catgtggccc tgaatcttcc atgtgcaact      720
ggccagggaa ggaaattatg gaaatagtca tcttgacat ntgc aaatga gatgcaaatc      780
ctggaagctc ttctaaaaaa aaa                                             803

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<210> 82
<211> 763
<212> DNA
<213> Cercopithecus aethiops

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<220>
<221> misc_feature
<222> (1)..(763)
<223> n is a, g, c, or t

```

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<400> 82
tcgtgcttta ccgtatcgcc gctcccgatt ccgagcgcac cgccttctat cgccttcttg      60
acgagttott ctgagcggga ctctgggggt cgaaatgagc tagcccttaa gtaaccgcat      120
tttgcaaggc atggaaaaat acataactga gaatagaaaa gttcagatcg aggtcaggaa      180
cagatggaac agggctgacc ggtcgaccgg tcgaccctag agaaccatca gatgtttcca      240
gggtgcccc aaggacctgaa atgacctgtg gccttatttg aactaacc aa tcagttcgct      300
tctcgcttct gttcgcggc ttctgctccc cgagctcaat aaaagagccc acaaccctc      360
actcggggcg ccagtctcc gattgactga gtcgcccggg taccctgtga tccaataaac      420
cctottgcag ttgcatecga cttgtggtct cgctgttcct tgggagggtc tctctgagt      480
gattgactac ccgtcagcgg gggctcttca gtagcccttc cttttagca aagacagaca      540
gatggtgac caagagatac gcaagaagag gaccgtgtgt gtaatgggtg agctctaaaa      600
agagaaatca cttggatgga aatgaaggag aggaaaaggc tgatgtggat ggctgggaag      660
aggttcgatg gttaccttgg caaccgagct tctttctcat cccatccctt ccctagtct      720
tgtcttaaaa gatttttttn tatgtccctt ccctcccaag ggg                                             763

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<210> 83
<211> 861
<212> DNA
<213> Cercopithecus aethiops

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<220>  
 <221> misc\_feature  
 <222> (1)..(861)  
 <223> n is a, g, c, or t

<400> 83  
 ttggggganc ctgtcagnac canttttact catatccgga tcctgacctt cattcagtgt 60  
 tctagattga aatcacagat tttggataga gaaaaaaaaa tattctctgc aatctaataa 120  
 aaccaacttt tttttttttt tttttttttt ttgagacaga gtcttgctcc atggcccagg 180  
 ctagagtga gtagcacgat ctgggcttgc tgcaacctct gcctgtcggg ttcaaccgat 240  
 tctcctgctt cctgtctect gcccagcct ntcaagtagc agggattaca ggcatgtgcc 300  
 atgatgccca gctagttttt tgtattttta gtagagatgg ggtcttgcca tgttgcccag 360  
 gctggacttg aactcctgac ctgaggtgat caggccatct tggcctccca aagtgttggg 420  
 attacaggcg tgagccatcc tgcctggcca aaaccagcat attttatgga taggaaattg 480  
 gaccaaaggc gaatctttta ttgcaggctg tgggnttttt ccatgtggct ggtggmacac 600  
 tgcaccaagc agcacacaca ctaggccagt ttnccttgca gaccagttg caatcccatc 660  
 tntnagccag gattctatta ggtctcnaca accnatggga atttagggng ctcanagntt 720  
 nngggtggga aaaggggact aacctnctg ggttnanggn ttttnaantg gncnncnct 780  
 ttggancngg ganatttatt nccaaaanng gnnnggntng tntnngggn anaaaccaa 840  
 ttttgggaaa aaancntttt t 861

<210> 84  
 <211> 767  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(767)  
 <223> n is a, g, c, or t

<400> 84  
 ggnattgncn agcggmtaac aatttcacac agnaattccg tatttgaaat ttggggacaa 60  
 tcgcttgaat cttaaaatta cttttctggt cagcgcgccc gaaggctctaa gcatttgtga 180  
 aatgtctttt tcccccccc ccaccccttg atgctgttct ctttgggctg tottaattac 240  
 acaggggttg agaaaccaa ttaaaattag gctgtcttgg tcaacagtga tcacgttgca 300  
 tgcttttagc tttgcttggt gaagttgctt ctctccctg agtggctttc ctctttttt 360  
 tttttttttt tttattttta aaaggaaata tcataagctc tttcagaaat actcacagga 420



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agtgagtgtc cgtatgctgg ttactcacca gcaactgant gttggcaggt ggagaatgct 480
accgcancn cccanacaga tctgcaaact gggccnttnc agangatnaa aacagggtgc 540
gtggaantan ggtttttggn naaangcant ttnaaagnaa atgggcactg cattnnnttc 600
nagggggggg anttaagnaa cangnttggg gtnaaaaagn ncntgnttcc attnngngg 660
tnctgctcct ttnaaanggg nggnnggttt naaaaaaag gggccncnc cccanaaaaa 720
aattttttgg nggaaaacct nccaaaaaaa anacccncn tttttgn 767

```

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<210> 85
<211> 761
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(761)
<223> n is a, g, c, or t

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```

<400> 85
cngcttgcca acctacaggt ggggtctttc aaaatatgct gttacaaata tcattttggt 60
gtatgtatgt caaaacaaaa actgccttta tgtcaatatg ctgtaaaaat ctatcagaat 120
atatcttaat tcttaacttt cattgttgtc tgtgggttgt cttgtataat tattatcaca 180
tctacagtat tttctgtagg taaatatgaa atgtattata aatgtaccag ggggaaaatg 240
ccctttaata agcctttccc tagacaaagc accatttagg cgtttagaag caagaactag 300
tgaaatcaga aattgctgtc atacatactc acctgtgaat ggtcgtacaa aggatcccaa 360
gcgcaggact tgtcctggaa gcagaggatc ggattccacc aggaaaagag gcaagtagaa 420
atgccaaatg ccagcgtcc ctttncctag ctcatcttat ttgtaggcac tcagattttg 480
gaatcctcca ggactaacat taaaacccca ctagggngtt tncctaatnc cgggaaanga 540
gncagtaggn caaacaactt atcccnncna nanaggaaca attccttgag ctcccnct 600
gtttcngaaa ccctnttccc ttntgggncc ctgnanaagg nctgccnaa tgctngggag 660
nccncnggt tttnatgaaa accatntnaa aatnccnaa agtnccccc ccaaggnaan 720
nttcnttta aanttttggg aaaaaaanc cctnanaaa n 761

```

```

<210> 86
<211> 791
<212> DNA
<213> Cercopithecus aethiops

```

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<220>
<221> misc_feature
<222> (1)..(791)

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<223> n is a, g, c, or t

<400> 86

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tnggggacca gcttgccaaa tctacaggtg gggctcttca aaatattgcg ttacaaatat      60
cattttggtg tatgtatgtc aaaacccaaa ctgcctttat gtcaatatgc tgtaaaaatc      120
tatcagaata tatcttaatt cttaactttc attgttgtct gtgggctgtc ttgtataacn      180
attatcacat ctacagtatt ttctgtaggt aaatatgaaa tgtattataa atgtaccagg      240
gggaaaatgc cctttaataa gcctttccct agacaaagca ccatttaggc gtttagaagc      300
aagaactagt gaaatcagaa attgctgtca tacatactca cctgtgaatg gtcgtacaaa      360
ggatcccaag cgcaggactt gtccctggaag cagaggatcg gattccacca ggaaaagagg      420
caagtagaaa tgccaaatgc cagcgctccc ttcccccagc tcatcttatt tgtaggcact      480
cagattttgg aatcctccag gactaacaat aaaaaccaca ctaggttggt ttcttaattc      540
ctgtgaaatg agtcagtagg tcaaacaact tatccactcc agagagagaa caattccttg      600
agctacactc cctgtttcca gtaacctat tccctctctg tgcctctgga taaagtgtg      660
ncnacaatgc atgganagcc cccgggttct gatgaaan cn atngaaagat ngcanaaagt      720
agctgcctta agggaangtt cccttngaaa tttaggnaaa aaaaocnnt aaaaanacng      780
gnggtcggtt t                                                                791

```

<210> 87

<211> 783

<212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc\_feature

<222> (1)..(783)

<223> n is a, g, c, or t

<400> 87

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ttggggancca gcttgccaan tctacaggtg gggctcttca aaatattgcg ttacaaatat      60
cattttggtg tatgtatgtc aaaacccaaa ctgcctttat gtcaatatgc tgtaaaaatc      120
tatcagaata tatcttaatt cttaactttc attgttgtct gtggggtgtc ttgtataatt      180
attatcacat ctacagtatt ttctgtaggt aaatatgaaa tgtattataa atgtaccagg      240
gggaaaatgc cctttaataa gcctttccct agacaaagca ccatttaggc gtttagaagc      300
aagaactagt gaaatcagaa attgctgtca tacatactca cctgtgaatg gtcgtacaaa      360
ggatoccaaag cgcaggactt gtccctggaag cagaggatcg gattccacca ggaaaagagg      420
caagtagaaa tgccaaatgc cagcgctccc ttcccccagc tcatcttatt tgtaggcact      480
cagattttgg aatcctccag gactaacaat aaaaaccacac taggtnggtt tcctaattcc      540

```

tgtgaaatga gtcagtaggn caannantta tncnctccag agagagaaca attccttgng 600  
 ctacactccc tgtttcnna acccnattnc ctttctgngn ccctgganaa aggggtgccc 660  
 anaatgcntg gggnnncccc ccgntcttg annaaaaacn tnttaaaaaan ngccnaaagt 720  
 anccctcnc nanggaagnt tcccccttta aattttnggn naaaaaannc ccttnaanta 780  
 ann 783

<210> 88  
 <211> 769  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(769)  
 <223> n is a, g, c, or t

<400> 88  
 ttggnattgn ccagcggnta acaatttcac acagnaattc cgtatttgaa atttggggac 60  
 aaacaaacat aactctttct ctttccttga aggggttaatg ctccaaccag cctcagattg 120  
 gttcgcttga atcttaaaat tacttttctg gtcacgcgcg ccgaaggctt aagcatttgt 180  
 gaaatgtctt ttttcccccc cccacccct tgatgctgtt ctctttgggc tgtcttaatt 240  
 acacaggggt tgagaaacca aattaaaatt aggcgtgtct ggtcaacagt gatcacgttg 300  
 catgctttta gctttgcttg ttgaagttgc ttctcctccc tgagtggctt tcctcctttt 360  
 tttttttttt tttttatttt aaaaaggaaa tatcataagc tctttcagaa atactcacag 420  
 gaagtgaagt tccgtatgct gggtactcac cagcaactga gtgttggcag gtggagaatg 480  
 ctaccgcagc cgcacagaca gatctgcaga ctggcccat tgcagangat tagacacagg 540  
 gtgcgtggat catanggggt tttgtacaga aggcagtttt aagangaaan tgggcactgc 600  
 atgtcatctc nangggngg tgattcangg ancanggctg ggggtnaaaa gcacctggct 660  
 gccattnngg agntcctgct aatttttaaa nggcagggtg gttttaaaaa aaaagctccc 720  
 ccccccccaa aaannnttt tttggaggna naacttccaa aangaanga 769

<210> 89  
 <211> 754  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(754)  
 <223> n is a, g, c, or t.

<400> 89  
 cagcttgcca acctacaggt ggggtctttc aaaatattgc gttacaaata tcattttggt 60  
 gtatgtatgt caaaaccaa actgccttta tgtcaatatg ctgtaaaaat ctatcagaat 120  
 atatcttaat tcttaacttt cattgttgtc tgtgggttgt cttgtataat tattatcaca 180  
 tctacagtat tttctgtagg taaatatgaa atgtattata aatgtaccag ggggaaaatg 240  
 ccccttaata agcctttccc tagacaaagc accatttagg cgtttagaag caagaactag 300  
 tgaaatcaga aattgctgtc atacatactc acctgtgaat ggtcgtacaa aggatcccaa 360  
 gcgcaggact tgccttgga gcagaggatc ggattccacc aggaaaagag gcaagtagaa 420  
 atgccaaatg ccagcgctcc ctttccocag ctcatcttat ttgtaggcac tcagattttg 480  
 gaatccteca ggactaacia taaaaaccac actaggttgt tttcctaatt cctgtgaaat 540  
 gagtcagtag gtcaaacaac ttatccactc cagagagaga acaattcctt gagctacact 600  
 ccctgtttnc agtaacccta ttcctctct gtgtccctgg ataaagtgt gcnacaatgc 660  
 atggggagnc caccgggttc tgaatgagac aatcgtaaan atngccaaaa nttagctgcc 720  
 ntcangggaa anttnocntt tgaaatttaa gnaa 754

<210> 90  
 <211> 866  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(866)  
 <223> n is a, g, c, or t

<400> 90  
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 ttctagattg aaatcacaga ttttgatag agaaaaaaa atattctctg caatctaata 120  
 aaaccaactt tttttttttt tttttttttt ttgagacag agtcttgctc catggccag 180  
 gctagagtgc agtagcacga tctcggttg ctgcaacctc tgctgtngg gttcaaccga 240  
 ttctcctgcc tctgtctcc tgcccagcc tntcaagtag cagggattac aggcattgtc 300  
 catgatgcc agctagtttt ttgtattttt agtagagatg gggctctgcc atgttgccca 360  
 ggctggactt gaactcctga cctcaggtga tcaggccatc ttggcctccc aaagtgttg 420  
 gattacaggc gtgagccatc ctgcctggcc aaaaccagca tattttatgg ataggaaatt 480  
 gaggcttaga tggggggaga aaaacattac acagattaaa ccacagctaa tgtcaagtgg 540  
 tgaccaaagg cgaatctttt attgcaggct gtgggttttt ccatgtggct ggtggtacac 600

tgcaccaagc agcacacaca ctaggccagt ttcctttgca gaccagttg caatcccatc 660  
 tntaanccag gatactatta ggtctcnaca ncctatggna ttttaggggtg ctcanagttt 720  
 aggggtgggaa aaggggacta anctncttgg nttaaggnt ntccactggg cccctncttt 780  
 nggnccnggg antttnatgc ccaaaaancgg tngggccttt ttgggggnan aannccaanc 840  
 cnngggaaaa aaacnttttt gttang 866

<210> 91  
 <211> 783  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(783)  
 <223> n is a, g, c, or t

<400> 91  
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 acaaacataa ctctttctct ttccttgaag ggtaaatgct ccaaccagcc tcagattggg 120  
 tcgcttgaat cttaaaatta cttttctggg cagcgcgcc gaaggctctaa gcatttgtga 180  
 aatgtctttt tccccccccc ccaccccttg atgctgttct ctttgggctg tcttaattac 240  
 acaggggttg agaaaccaa ttaaaattag gcgtgtctgg tcaacagtga tcacgttgca 300  
 tgcttttagc tttgcttggt gaagttgctt ctcctccctg agtggctttc ctcctttttt 360  
 tttttttttt tttattttta aaaggaaata tcataagctc tttcagaaat actcacagga 420  
 agtgagtgtc cgtatgctgg ttactcacca gcaactgagt gttggcaggt ggagaaatgct 480  
 accgcagccg ccagacaga tctgcagact ggccccattg cagaggatta gacacaggt 540  
 gcgtggatca tanggttttt gtacagaagg cagttttaag aggaaattgg tcaactgcatg 600  
 tcatctcgag gggtggtgat tcaaggagca gggctngggg gtcanaangc acntggctgc 660  
 catctcgggg gttcctgctc acttntnaaa gggcaggctg gcttntaaaa anaaatgctn 720  
 ccttcacccc caaanaggga ttttttttgc agngaataac tccccaaaaa tgaatngccc 780  
 cna 783

<210> 92  
 <211> 775  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(775)

<223> n is a, g, c, or t

<400> 92

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ttggggaanc agcttgccaa anctacaggt ggggtctttc aaaatattgc gttacaaata      60
tcatttttgt gtatgtatgt caaaaccaa actgccttta tgtcaatatg ctgtaaaaat      120
ctatcagaat atatcttaat tcttaacttt cattgtgtgc tgtgggttgt ctgtataat      180
tattatcaca tctacagtat tttctgtagg taaatatgaa atgtattata aatgtaccag      240
ggggaaaatg ccctttaata agcctttccc tagacaaagc accatttagg cggttagaag      300
caagaactag tgaaatcaga aattgctgtc atacatactc acctgtgaat ggtcgtacaa      360
aggatoccaa gcgcaggact tgtcctggaa gcagaggatc ggattccacc aggaaaagag      420
gcaagtagaa atgccaaatg ccagcgctcc ctttcccag ctcattctat ttgtaggcac      480
tcagattttg gaatcctcca ggactaacia taaaaccac actaggttgt tttcctaatt      540
cctgtgaaat gagtcagtag gtcaaacaac ttatccactc cagagagaga acaattcctt      600
gagctacact cctgtttcc agtaacccta tccctctct gtgtccctgg ataaagtgt      660
gccaanaatg catggagagn ccccggtt ttgaatgana cccatcgtaa agatngccaa      720
aagntagctg cctcaaggg aagttncnt ttganattta gnagaaaaag tccnt      775

```

<210> 93

<211> 837

<212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc\_feature

<222> {1}..(837)

<223> n is a, g, c, or t

<400> 93

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ttngggganc tagcttgoca aanctacagg tggggctttt caaaatattg cgttacaaat      60
atcatttttg tgtatgtatg tcaaaaccaa aactgccttt atgtcaatat gctgtaaaaa      120
tctatcagaa tatactctaa ttcttaactt tcattgttgt ctgtgggttg tctgtataa      180
ttattatcac atctacagta ttttctgtag gtaaatatga aatgtattat aaatgtacca      240
gggggaaaat gccctttaat aagcctttcc ctagacaaag caccatttag gcgttagaa      300
gcaagaacta gtgaaatcag aaattgctgt catacactac cacctgtgaa tggcgtaca      360
aaggatccca agcgcaggac ttgtcctgga agcagaggat cggattccac caggaaaaga      420
ggcaagtaga aatgccaaat gccagcgtc ccttnocca gctcatctta tttgtaggca      480
ctcagatttt ggaatcctcc aggactaaca ntaaaacccc actagggggn ttncnnantc      540
ctgngaaatg agtcagtagg ncaaacannt ttncnctcca nanannnaan antcctgggn      600

```

ntacnctccc tgnttcagna acccnattcc ctncntgggn ccnggnaaaa gggcgnccca 660  
aatgggnnggg ngmcccccg nttntnanga aacctatntt aaaatttccc aaaantttnc 720  
nccccnnann gaaannnncc nttttaaatt ttnggananaa aaancocnt naaaaaana 780  
ngggggcggn tttntttttt aaagaaanaa anattttttt ttnggggagg ggttnt 837

<210> 94  
<211> 837  
<212> DNA  
<213> Cercopithecus aethiops

<220>  
<221> misc\_feature  
<222> (1)..(837)  
<223> n is a, g, c, or t

<400> 94  
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tagattgaaa tcacagattt tggatagaga aaaaaaata ttctctgcaa tctaataaaa 120  
ccaacttttt tttttttttt tttttttttt gagacagagt cttgctccat ggcccaggct 180  
agagtgcagt agcacgatct cggcttgctg caacctctgc ctgtcgggtt caaccgattc 240  
tcttgcctcc tgtctcctgc ccagcctct caagtagcag ggattacagg catgtgccat 300  
gatgccagc tagttttttg tatttttagt agagatgggg tcttgccatg ttgccaggc 360  
tggacttgaa ctctgacct caggtgatca ggccatcttg gcctcccaa gtgttgggat 420  
tacaggcgtg agccatcctg cctggccaaa accagcatat ttatggata ggaaattgag 480  
gcttagatgg ggggggaaaa ancnttnc cc aaattaancc acagcttatg tnaagtgggt 540  
  
gncccaggcg gncnnnctt tggncnttt tcttttgaa ccngntgca atcccccttt 660  
taanccggga atcttttggg tttcncncc cttgggnatt nngggggccc caanttnngn 720  
nggggnaagg ggnaaaaacc cctttggntn agggntttaa aanggggncc ccttttggn 780  
cngggnttt tntnccnaan ngggnggggt ttttbtngg annaacnncn acnnggn 837

<210> 95  
<211> 812  
<212> DNA  
<213> Cercopithecus aethiops

<220>  
<221> misc\_feature  
<222> (1)..(812)  
<223> n is a, g, c, or t

<400> 95  
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 acaaacataa ctctttctct ttcttgaag ggttaatgct ccaaccagcc bcagattggt 120  
 bcgcttgaat cttaaaatta cttttctggt -cacgcgcgcc gaaggtctaa gcatttgtga 180  
 acaggggttg agaaacaaaa ttaaaattag gcgtgtctgg tcaacagtga tcacgttgca 300  
 tgcttttagc ttgcttgtt gaagttgctt ctctccctg agtggctttc ctctttttt 360  
 tttttttttt tttattttaa aaaggaaata tcataagctc tttcagaaat actcacagga 420  
 agtgagtgtc cgtatgctgg ttactcacca gcaactgagt gttggcaggt ggagaatgct 480  
 accgcagccg ccagacaga tctgcagact ggccccattg -cagaggatta gacacaggg 540  
 gcgtggatca tagggttttt gtacagaagg cagttttaag angaaattgg tcaactgcatg 600  
 tcatctcgag ggggtggtgat tcanggagca gggctggggg tcanaangca cgtggctgca 660  
 tctcgnggt nctgctcant tttaaaggn ngctggnntt aaaaataang ntnttcacc 720  
 ccaaaangaa ttttttgcag gnaaannttc naaaaganna ccnntttt tgnnaaaacn 780  
 tgggaaancc ccntttnaan gmggnnttta an 812

<210> 96  
 <211> 805  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(805)  
 <223> n is a, g, c, or t

<400> 96  
 ttgggggancn gcttgccaan tctacagggtg gggctcttca aaatattgcg ttacaaatat 60  
 cattttggtg tatgtatgtc aaaacaaaa ctgcctttat gtcaatatgc tgtaaaaatc 120  
 tatcagaata tatcttaatt cttaactttc attgttgtct gtgggttgtc ttgtataatt 180  
 attatcacat ctacagtatt ttctgtaggt aaatatgaaa tgtattataa atgtaccagg 240  
 gggaaaatgc cctttaataa gcctttccct agacaaagca ccatttaggc gtttagaagc 300  
 aagaactagt gaaatcagaa attgctgtca tacatactca -cctgtgaatg gtcgtacaaa 360  
 ggatcccaag cgcaggactt gtccctggaag cagaggatcg gattccacca ggaaaagagg 420  
 caagtagaaa tgccaaatgc cagcgtccc tttcccagc tcatcttatt tgtaggcact 480  
 cagattttgg aatcctccag gactaacaat aaaaaccaca -ctagggtgtt ttcctaattc 540  
 ctgtgaaatg agtcagtagg tcaaanaact tatccactcc agagagnгаа caattccttg 600



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agctacactc cctgtttcag naacctatt ccctctctgg gtccctggat aaagggctgc      660
cacaatgcat ggggagcccc cnggntnttg atggnaacac tcntaaaaat tgccaaaagn      720
ttnctgcctn aangaaaant nccctttnaa ttttggana aaaaanccct tnaanaaacn      780
ggggggcggt ttttcnttaa agaaa                                           805

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<210> 97
<211> 854
<212> DNA
<213> Cercopithecus aethiops

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<220>
<221> misc_feature
<222> (1)..(854)
<223> n is a, g, c, or t

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<400> 97
ttggggaacn ngcttgccaa ntctacaggt ggggtctttc aaaatattgc gttacaaata      60
tcattttggt gtatgtatgt caaaacaaaa actgccttta tgtcaatatg ctgtaaaaat      120
ctatcagaat atatcttaat tcttaacttt cattgtgtgc tgtgggttgt ctgttataat      180
tattatcaca tctacagtat tttctgtagg taaatatgaa atgtattata aatgtaccag      240
ggggaaaaatg ccctttaata agcctttccc tagacaaagc accatttagg cgtttagaag      300
caagaactag tgaaatcaga aattgctgtc atacatactc acctgtgaat ggtcgtacaa      360
aggatcccaa ggcgaggact tgccttgga gacagaggatc ggattccacc aggaaaagag      420
gcaagtagaa atgocaaatg ccagcgctcc ctttcccag ctcattttat ttgtaggcac      480
tcagattttg gaatcctcca ggactaacia taaaaaccac actaggttgn tttcctaatt      540
cctgtgaaat gagtcagtag gtcaaacaac ttatccactc cagagagaga acatttcctt      600
gagctacact ncctgnttcc agtaacccta ttccctctct gggtccttgg ataaagggct      660
gocnacaatg catngggggg cccccgggt tntgaangaa aanntnntt aaaaatngcc      720
aaaanntaac tncctcaan ggnnannnnc cccttttnaa ntttttgggn aaaaaaanc      780
cccntnaaaa aananagggg gggnggnttt ttttttnnaa aanaanaann aanntttttt      840
tttggggnan annt                                                         854

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<210> 98
<211> 912
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(912)

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<223> n is a, g, c, or t

<400> 98

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ttttgttggt ggggnntgna gcgncggctn aacttttttg cacacagaaa ntcacaggaa      60
cacaggagtc agtttcttca gcaangtctt gcttgtecng ttntgaacgg taggatnttg      120
tcgctatatt tgnacacatg agggacctnt gtggagcttc caaatagtgc gctnggcgca      180
atatnnacaa ganacagccc ttagcgantg gcttggtgnt gggngagatg ntgctctgtg      240
ngatgaattn acanacaca gagttttttn ttgnntgct tgtttctgt tntnaacgg      300
ggatttgtn ttttggacca tgggatntct atgggctnan agangtccta tgtgagaata      360
nggcaatgta ctgcctttna naactggaat gangctnggt gagaantgc tctgtgttct      420
gtganttccg tactntgaaa ttgggggaen aacaaacata nctctttttt ctttctcttg      480
aagggnataat tgttccaacc ccgcncaga ttgggntngc ttgaatctta naatncttt      540
tctggtcccg ccgcgcgang gtnagcttt tgnngaaatg gtnttttttc cccccccca      600
ccccttggtg gngggtnntt ttgggcttgg nnttnanntn ccccggggg nntngnnna      660
ccnatttttn attttgggn ntttgggnc ncanggggtc cnnnnnnnnn gmctnntnann      720
cttggttgn nngaangntg nttntcccc cccggggggg tccccccnt ttttttttt      780
ttntttttt ttttnagggg antttntng tctttttna annncncgg gntgggggg      840
tcnnttttt gtttttnncn nnnnttggn nngggggggg gganntttct ctnnnncccc      900
cnnnttttn gc      912

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<210> 99

<211> 807

<212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc\_feature

<222> (1)..(807)

<223> n is a, g, c, or t

<400> 99

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ctgcttgcca anctacagg ggggtcttcc aaaatattgc gttacaaata tcattttggt      60
gtatgtatgt caaaacaaa actgccttta tgtcaatatg ctgtaaaaat ctatcagaat      120
atatcttaat tcttaacttt cattgtgtgc tgtgggttgt cttgtataat tattatcaca      180
tctacagtat tttctgtagg taaatatgaa atgtattata aatgtaccag ggggaaaatg      240
ccctttaata agcctttecc tagacaaagc accatttagg cgtttagaag caagaactag      300
tgaaatcaga aattgctgtc atacatactc acctgtgaat ggtcgtacaa aggatcccaa      360
gcgcaggact tgtcctggaa gcagaggatc ggatccacc aggaaaagag gcaagtagaa      420

```

atgccaaatg ccagcgcctcc ctttnccag ctcatttat ttgtaggcac tcagattttg 480  
 gaatcctcca ggactaacan taaaacceca ctagggtgnt ttcctaattc ctgtgaaatg 540  
 agtcagtagg tcaaanannt ttncnctcca ganaggaaca attccttgag ctanctcct 600  
 gtttcaggaa cctattccc ttntgggncc ctggaaaang gctgccacan tgctgggaag 660  
 cccccgggt tnaangnaaa aatcnnaaaa ttgccaaaan tancnncccn agggngngtn 720  
 cccttanant tttinggaaaa aancoccnta aaaaancngg gngcgnnttt tnttaaaaa 780  
 aaanaaattt ttnttngggn gntttnn 807

<210> 100  
 <211> 814  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(614)  
 <223> n is a, g, c, or t

<220>  
 <221> misc\_feature  
 <222> (1)..(814)  
 <223> n is a, g, c, or t

<400> 100  
 ttggnattgn ccagcggnta acaatttcac acagnaattc caggcacagt tggctgtaa 60  
 ctagaatagt aagtggcttc ctaggctctg tcaactcctaa actgtagggg gcttcagcc 120  
 tcggagatta cggaagtagt acttttcatt agcaagctca agaagaagtg tcaaaatagg 180  
 atgacacttt cctagtcgct ctgcaaaaac ccaaaaacc agaaggggtg tcatctagac 240  
 actcctaagt ctatgcaggt gtcagcctgc cctcacccaa caccagccag cagcgtgcac 300  
 cattcaacca tatcttaact tgccccttac aaattgacac ttacactaac aagcccttg 360  
 atctcatttg tttaaaatga cagatatata accctcacgg gggttccac tcaaggcctt 420  
 ncagcctncc nccgtccct gncaccccc aaacctacac acgtgttagc ccgacaccgg 480  
 cccacaccgg tcccacgtgc acctgggtcta acacactncc cagctgtggg cgcgccacgg 540  
 gctttctnan gtagctgang gncccccct gatccccggt tntccaaaan aaaaaaacgg 600  
 gaaggacaag ggcccttttc nccngngncc caacctnngg gggggngngt ccaacccctt 660  
 tnttnntat aaaccccaaa aaananaaag ggcccggggn ccncccccc ccttnaaaaa 720  
 nccgncccc cnttttnccc ccnaaaaaa nggggggaaa aaaaaaattt aaaaaaannc 780  
 nttttttnt tttncccccc ccnccatnta nata 814

<210> 101

<211> 756  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(756)  
 <223> n is a, g, c, or t  
 <400> 101

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tggtcccaga gtctaaatag gagecccaaa ctaatcactg tatggtagtc gaacttcccg      120
gcacttcccc gacaatctac aaocccatcc aaaggggtca gaaactggta ataaaaatacc      180
agctatgagc ctntccttcc cctcaagaga tctatcaatt cggcctcacc ttoccacctc      240
tagcctgcgg gaacaaacat cccaggatcc cgggcggttt cgattgacgt tacttccggg      300
aaaagtaacc ttgcttcggc ggttgccggc ctgaaaagct ctgcgcacat ttccctccgc      360
nagatctgct tgctcactgt agcgatgaca tcctcctcct cctccccgcc gcctttcggc      420
aatcttcgcc agtcccagcc ccgaccaatc tgtactcaga tggcatggat caggggtctc      480
cctcgaaccc cgggttcgcac ggggcgctag gtggcagcgg cggggtgcga gctgcgcgag      540
gccnacngca gcggcactgc gggtgccng gggcaggcca caagcantga ntgtnggecg      600
ggccgggggn aaccacccg ntagcgggt cnantgnttc tggcctggt ttngngcct      660
tttctcccc ccncanggt tcccgggnnc ctgttncgt tcttttaann ggggaaaggg      720
gcccccccc ccccnngcca angcccnnn acnnnt      756

```

<210> 102  
 <211> 804  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(804)  
 <223> n is a, g, c, or t

```

<400> 102
tggnntgncc agcggntaac antttcacac agaattccaa ttatggggaa caagacatct      60
gaattggcta aaactccttg cagcagcaaa aaggaaaagc aaaacaaaac catacatgtg      120
gtttctgtct ttgcttcctg tcttttcttc cacttactc ctcttcccc ttcctcttc      180
ccttccccct ccccatcttt gctacaaaa aaaaatctag agaagccttc tattaacctg      240
aaccctttaa agaagtcaga acaaaggcac cacttgccgc tttttgggat gtcgtgttt      300
ctttatggag ttttcaagag taatgggcag atgcttttag gtctacagtt ctgctttcct      360

```

gtattgcact acctgattct ttgacttttg gagataccag aaattacctt gtaccatgag 420  
 aggatttggc tttggcatgt gtaatggcag atgagagcta caaagttaag agtggctgaa 480  
 gatggtttac atgaagtggg cttaggtggg ttagctgagc tcccaggaag ttgttgtcta 540  
 ggatcccaat tctagttcag aggtgcattc ctattattat tatcattact attgggtggg 600  
 ntgntattat tttgagacag agtcttgctc tgtaoccca ggctggagtc ctctggcacc 660  
 attacgggtg actggagcct naanttcag gctncagaga tectectttt annctcnnag 720  
 tagtgggacn canangnngg nnecccccaa cnnannnatt tttgnncttt tgnanaann 780  
 gggtttgntt tttngncnnn ntgn 804

<210> 103  
 <211> 795  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(795)  
 <223> n is a, g, c, or t

<400> 103  
 ggnattgncn agcggntaac aatttcacac agnaattctg gagttagggt gtctgggcta 60  
 ttcaattagt ttctatgtgt ctgacacatg gcagaaactt attaaatgct tgaatgaata 120  
 cataaagcaa gatgacagtt tcagaatgna ccaggtaatt caaagtactg aatccatatt 180  
 aaattttatt tagtctacac agaagtgaag taacactaaa atctgggcct ttaccaggtg 240  
 atggcaagta ttcatttcca tcatccagcc cgttacctgg cacatagtta ctgccctatg 300  
 taaatgctta tcacagcaat caatcaatga aatgtttttc tcatagagtt cgggtgaataa 360  
 ctacagacag catactcaca gaggattcaa agagtatttg acttgatat attgttttaa 420  
 acagttggaa cctgataatg cagttttcta aaatacagtg aaagggcttg tcctaaaggg 480  
 catgtcagga tatgtgtgag aaaggatgaa cttgtcctgt gaagacaacc ttgcattagc 540  
 tctagcagaa tgagccattg cctacctggg ctggggaagg cggcacctca gtatctcct 600  
 cacctgctcc ctggcacttt aaatccctct gtgaagangt cagttgtaat tttcagtaag 660  
 attgaagggt tcaaagcact gacccttggg gggaatggat tngcttaagt tggctctgaa 720  
 ngaagnggct gggatnngct ntctganaaa cccgggattg tgaggnaatg gagacngccg 780  
 ggagggttna anaaa 795

<210> 104  
 <211> 641  
 <212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc\_feature

<222> (1)..(641)

<223> n is a, g, c, or t

<400> 104

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tgggggnacc cagcggntaa cattttcaca cagaaatctc attcaatgaa ctgttatggg      60
gtctcacatt gtaccaggca ctggggattc agcttccagt tcatagtctg catgcaaacc      120
gacatgcagg tagacatgca gacagaaaat cggaacgcaa cacggtaagt gctatgctag      180
agaatgagaa ggactgtcag taatcacaac cacctttcac tgggttcctt cagtgtgcc      240
ggctcgtgta cattattttg tttagtgtc acaattgtat ggactgtgta ctatcatttg      300
ccagattata tggatgaaga aactagactg aggggggttaa ataactcgtc caagatcatg      360
cagacaaaaa accacagaga ttattttcca atacaaactc tctggctgta cagctcaagt      420
tcttaaacac tgggccaacc agtctgaatc tgagaggagg cattctaagg cttaacaggta      480
agtgggaatt gaaaggggtg agggaagcct tctggaggag atgccattac actgaatggt      540
gaatgagtag gagttagcta tctccagagg ggtagtggct gtgaaggggc gaggggtana      600
gggtgggaag gggatgatgg aaggtggtag agtggnnaca g                          641

```

<210> 105

<211> 757

<212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc\_feature

<222> (1)..(757)

<223> n is a, g, c, or t

<400> 105

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cngncttgcc aacctacagg tggggctctt caagatctgc tgacagtgaa gctaaatctg      60
gcggaagcaa aggattcact ttctcataat ggattaactc atcctatttg cctcttaaac      120
aatgggtatt ttaaagacag aagttgaagg aagtccaagt atccaatttt aaggatgcct      180
attagagcag ttataagaga gtgtctctct ttctctctct tctttcttct tcttggtagg      240
agtatgcagg aggtcattta aaagccagat agtgatacaa atcacaatgc agaaaaacat      300
ccccgtggac tcctccctgt cctatgtttg acattcttaa aatctatgtc ccaggctctg      360
aaatctttaa ataacttacc atgttctttg gcctgccctg ggaaatctat ttcagtaacca      420
gagctatgct ggttacacac cttttctgac tcatgttccc aagtgatttt attccagata      480
cgatttgggg acagttacgt gtactgttct gatattctcc taaaaggaaa ttatttttgg      540

```

aagtaaagtc actgataaaa tcanctcagg aaaatgcact ttgtaaatat taaaatataa 600  
 acttttttnaa ggnctgtctg gaaaanacta attgattttc ctgggnagca gttccatnga 660  
 acanccgatng atcttttaggg ggnagtgaan ggccccnatt tgaaaaangg gggcgggaaa 720  
 ngttcaaata ntttttccaa angggnnccct anntnnt 757

<210> 106  
 <211> 640  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(640)  
 <223> n is a, g, c, or t

<400> 106  
 ttgggggnanc gagcggntaa cattttcaca cagaaattca ttcaatgaac tggtatgggg 60  
 tctcacattg taccaggcac tggggattca gcttecagtt catagtctgc atgcaaaccg 120  
 acatgcaggt agacatgcag acagaaaatc ggaacgcaac acggtaagtg ctatgctaga 180  
 gaatgagaag gactgtcagt aatcacaacc acctttcact gggttccttc agtgtgccag 240  
 gctcgtgtac attattttgt ttagtgctca caattgtatg gactgtgtac tatcatttgc 300  
 cagattatat ggatgaagaa actagactga ggggggttaa taactcgtcc aagatcatgc 360  
 agacaaaaaa ccacagagat tattttccaa tacaaactct ctggctgtac agctcaagtt 420  
 cttaaacact gggccaacca gtctgaatct gagaggaggc attctaaggc ttacaggtaa 480  
 gtgggaattg aaaggggtga ggaagcctt ctggaggaga tgccattaca ctgaatgttg 540  
 aatgagtagg agttagctat ctccanaggg gtagtggtg tgaangggcn aggggtaaag 600  
 ggtgggaagg ggatnatgga aggggttnaa tnggncnng 640

<210> 107  
 <211> 818  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(818)  
 <223> n is a, g, c, or t

<400> 107  
 ttggggacca gcttgccaat tctacaggtg ggggtctttca agatctgctg acagtgaagc 60  
 taaatctggc ggaagcaaag gattcacttt ctcataatgg attaactcat cctatttggc 120

```

tcttaaacaa tgggtatttt aaagacagaa gttgaaggaa gbccaagtat ccaatttttaa 180
ggatgcctat tagagcagtt ataagagagt gtctctcttt ctctctcttc tttctttctc 240
ttggtaggag tatgcaggag gtcattttaa agccagatag tgatacaaat cacaatgcag 300
aaaaacatcc ccgtggactc ctccctgtcc tatgtttgac attcttaaaa tctatgtccc 360
aggtcttgaa atctttaaat aatctaccat gttctttggc ctgccctggg aaatctattt 420
cagtaccaga gctatgctgg ttacacaact tttctgactc atgttcccaa gtgattttat 480
tccagatacg atttggggac agttacgtgt actgttctga tatcttcta aaaggaaatt 540
atthtgggaag taaagtcaact gataaaatca actcaggaaa atgcactttg taaatattaa 600
aatataaaca ttattaaagg ccatgctgta aaaatactaa ttgattttcc tgggtagcag 660
ttacaataga acancgatng atctctaagg ggagagtgaaggacctcan ttganaaac 720
gtgaggcagg aaaagnttca aatnattatt tncaanaggg ntccctaagt tgttncttaa 780
anaaaaatttt tttcntnaaa aaaaaacnnt aanggccca 818

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<210> 108
<211> 608
<212> DNA
<213> Cercopithecus aethiops

```

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<220>
<221> misc_feature
<222> (1)..(608)
<223> n is a, g, c, or t

```

```

<400> 108
ttgggaccct gtcagaccan ttttactcat atcggtccc ctgaggctcg gagatcaaga 60
ccaccctggc caacatggtg aaaccctgtc tctactaaaa tacaaaaatt agccaggcgt 120
ggtaggcaggc gcctgtaatc ccagctactc aaaggctgag gcaggagaat cgcttgaacc 180
taggaggcag aggtggaagt gagccgagat cataccactg cactccagcc tgggcatcag 240
agccagactc tgcgcacaaa aaaaaaaaaa aaaaaaaaaa attagctacc tctccatcc 300
anaaatgaga gtcgaggctt ctgacttccc gggctcaatt tatctctccg cctcagcctc 360
ttgaggaact gggactacag acgtgacta tcacacttgg ctaatttttt tgagatgatg 420
tcttgtcttg tggccaggct ggagtacagt gacacaatct cagctcactg caacctccgc 480
ctnctgggtt caaccgatcc tnttgcttca gcctcccaag tagctgggat tacaggcgtg 540
ccccacaacg tccagntatt tttgtatttn aagnagagac nggggnnncc cctgttggnc 600
ngggngggg 608

```

```

<210> 109

```



<211> 516  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(516)  
 <223> n is a, g, c, or t

<400> 109  
 nggganccctg nccagnacct ttttactgca tatcggatcc tgagaagctc ctgatattcc 60  
 ctcaagccta aggcaaagta gtattcagaa cctcctatcc cactgactcc gagagocctgt 120  
 cctccgatat ctccaagaga gcctatcctc cgataggagg ggaagccctt ccaacctgca 180  
 ggtatcctcc ccagactcac catttctccc accccacact ggtggcttcc aaactttccc 240  
 tctcataaca aggcgccctg tcaccagac tgcttcctc ggcttgagga ggaggggaag 300  
 gcgcacgaag taggaaggaa cttggggaga gggcgggcgg aggggtggcg aagcactgag 360  
 gggagggcgg tgaagaaggc agaagtcagg cagtgaaggg gagaagcggc gggggcaggt 420  
 gagggcgggg gagtggggat ggggcgggg aaaggggccg agaggacgcg gagggggcag 480  
 aggtagggna caggagggga ggggaggggg agggcc 516

<210> 110  
 <211> 802  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(802)  
 <223> n is a, g, c, or t

<400> 110  
 tnggggaacc tgccagacct tttttactca tatcggatcc ttattgcctg gctatttcag 60  
 cctgggaggg gtttggttg aatatccctg gggaggcagg ctctcagggc taaaatagtg 120  
 ggagaaaaga ttaaaccctt aggaaactgg tacacatcag cgctaagtgt gactcagggg 180  
 gaaacaagaa ctaggacact tattactcca aaggagtgt atttggttca actcttgat 240  
 tttcttatta aaacttttgc aaagtgggtt gagaagaaag tgttacttcc agtggttacac 300  
 cctcaacact ttttcctgtg gagactccag catgttcatt atgttttctg aagccatggc 360  
 actgtagtac tctttcattg ttgttattat tatttaataa tataaaatga gacatttttg 420  
 ctccattttt cattcatatt ttgtcctaa ttacttttta aatatattct ggtgtcaggt 480  
 caatatttat agtctaacgt ttaagactta gactttggtt cttaggatgt tatttttgaa 540  
 tcagctgcgt ctggtaagg taaagatatt gaaagtgcct tgtaaattgt ccagtggcat 600

```

aaaagtattg tcatatcttt atgacataaa agaaaantgt tttcttcttt ttagcatgga      660
aaactttaca anccatttgc tggtagcngg ngangncctn ggggttggat ttcattgattt      720
tgggggtccct tgaggggtoca aantaccntt ctaanagnng aaanttttca nnaattcatg      780
antgncctna ttnaaanann tt                                              802

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<210> 111
<211> 851
<212> DNA
<213> Cercopithecus aethiops

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<220>
<221> misc_feature
<222> (1)..(851)
<223> n is a, g, c, or t

```

```

<400> 111
tacttttttt tgggggnncc aagncggnta acattttcac acagaaatct ccaagttccn      60
naggaccgca gnatectccc cagaaccocct gngaccaagt cactgtgggtt ggntgtgctg      120
ggcatccctg aggcccagcc actcaacttt actgggtcca ggattctata gaaagggaaa      180
ggggtagaaa atctcaaaag gcttcttcct ttcagggagg gggttccctc tcagcggctt      240
ctggaatctc taccactcc agccgacttt tgaggccatg tggtcctgga acaaggeccc      300
tctgagggcg gcagatgggg caggcggccc aggcacacag catggttggc tctgcggccc      360
agggcccaca aaagccttat tgagtcacca ccagcccccg gcagaggctg aggtggcagt      420
ggcgccgagc gcctgccacc taatgactgt cctggcacag ccagatgttc cgcagacctc      480
cggagcagcg ggaccaaggg cccgcccggg ccagccggca ccngannagg ccacttttaa      540
tttccaatta accagntttc agnntgancn aaanaggggg gcagtnggtg gneccacccc      600
cgggcnagta ngccccggcc cnnaaaannc cttnccaagt tntaanactn ccnatntga      660
aacnccacc nccngaatt ccnatggaa aaantggccc ccagccangg gcaagggntt      720
gggncctttc tttcttttg aaaaggaaat tttggttntt ttnacnaagg ccccceang      780
aaccccnatt t                                                              851

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<210> 112
<211> 773
<212> DNA
<213> Cercopithecus aethiops

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<220>
<221> misc_feature
<222> (1)..(773)

```

<223> n is a, g, c, or t

<400> 112

```

cagcttgcca antttacagg tgggantctt tcaagagcag taaaacgacc tatccaagga      60
aactcagcta gtaaaggcag ggacagggtg tgcaggctc tcggaactca cgagtcocccg      120
ccaggcgcat ggccgctcct tccccccggt gggcgtggcc aggccaggcc cgtccctcc      180
cctgagcgcg ttcctggcag cccggccggc cgttttctgc ctgcgtcgct gggcgcgcg      240
gcggggcgggc agcccatctg gcggccccc cggggcgggc cggggaggcg gccagactt      300
gctggagcca ggcgcctgcc cggggggccc cctgccgcc tggagaacct aggtgtggcc      360
gcggcggggg tggggggtgg tgctttcctt cccgctcgct cggctcttnc tgacgcacga      420
gggcaggatg cagcctcctc ccgtcctctc ctggcctcc gctcccgcg ccctggccc      480
gaatcctgga gggaatccaa acgcggggcg gggaggccgg ggcaggcccc tgaggccccc      540
ccccgatag ccatttaata ccaccgaag tcttgaccgt atttttgggg tgaccanct      600
tcctgtcttg ggcaagacca gctgaactct gacctnctgg anggccgatt ttaccttgc      660
cctcagggac ccnnaaatga tcgtaggaac cngnntcact actgctgtaa gccanancg      720
ttganatatn caattattca gcggnntcaa gtcccggaag cggnttttna cna      773

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<210> 113

<211> 807

<212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc\_feature

<222> (1)..(807)

<223> n is a, g, c, or t

<400> 113

```

ttgggggtgc gagcgntaa cantttcaca cagaattctt cagtgaattt cttaagccct      60
gagcatcttc tttgtattct gctttaagaa cttgtttgtt tctgtatttc atactcagtg      120
gctctggcgc ttggatgccc tggccccaca gaaggccttg aatactgaat ctgaggatgg      180
ggcttgctta taaggacctt actocctgct ttaaccagat tgtgttttaa cctttcatct      240
cactttttac ttttcattca tggatagtgt ttgtcactgt gtgtgtgtgt gtgtgtgtat      300
gaatgagtga atgaatatct ctacactct aaattctttt aaaggcagga agtactgttc      360
tcttgtttgc tattttatcc actctgctc tactgggtct ggcacataat aaagaaagaa      420
tgaacaggac aaacacccat tctgaaagtg aacttctctg gcaattgtcg tttgtacata      480
ccagctggag catagacaat tggcttttaa tgtggtaagg gaaaaggcca aaaaaagaat      540
cgtcattgac caagggttc accagatgat ttataatca nbccnaaagg gnctttnaan      600

```

aaaaaaggcc ttngaggaac aaatttnttc cnnntggaaa antgntttna aattttntn 660  
 gaaaaagttt tnanaatttt tgnaaaaccc ccccccnnt gaaaacntnt aaancnngna 720  
 annngnnnng ggcggggttt naaaaaaaaa aantcccccc cnnnaanng ggnctttnaa 780  
 aaannnnngn ntntctaaaaa aangggg 807

<210> 114  
 <211> 836  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(836)  
 <223> n is a, g, c, or t

<400> 114  
 ttggggacca gcttgccaan tctacagggtg gggctcttca gtatgtgtca agagtcagaa 60  
 tttaaagaag ataagaaaat taaatacact gagaacaatg catctcntga cattcaaaat 120  
 atgtaagtgc agcaaccagc agtaattcca taggcctttt atcaaccttt gccaaaacct 180  
 ataaaaagaa tatctaaaat tgctttttta tgaaagttcc tatttattct tgtttccctt 240  
 accagagagc ctgctttccc ctactgatg agaacacagg gggctcctggg taaagagtcc 300  
 ataanattta aaaaggagta tgccttgccc tcccatgacc ctcttacttc acaataaggc 360  
 catcttttac ctgggtttaga ttgcagact aggtccatta gatacgttgt cattaaatc 420  
 ctatactata cctaataatt tgtaatcttg acaggtatta ttttcatttt atagacagat 480  
 ctaggaaaat tacatgactt atcggaatcc cttcaaatat cacagagcaa agtcatgatt 540  
 ttaacttggtg ttgcccactc tgaaactcac actggaattc gagactagtg tgcgtaacat 600  
 ggcgaaaccc catctctatt tntnttttc aaaatntntt tttccaaaat ttgctggggg 660  
 tgttggtgtg tgctgtant ncagcctnct tgggaggctn aanngngnga cngcttgacc 720  
 ctggngnaa aggctaaatn gncttnttn gccctggan ttaaccnngg ggaaaaangg 780  
 aaccttntc aaaataaatt ttaaattaaa naangccnag gtttccccna aaaaat 836

<210> 115  
 <211> 839  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(839)  
 <223> n is a, g, c, or t

&lt;400&gt; 115

```

ttgggananc gagcggntaa ctttttcaca cagaantcca gtgtgagttt cagagtggca      60
aacacaagtt aaaatcatga ctttgctctg tgatatttga agggatccg ataagtcag      120
taattttcct agatctgtct ataaaatgaa aataatacct gtcaagatta caaatattag      180
ggtagtat aggtatttaa tgacaacnta tctaattggac ctagtctgca aatctaaacc      240
aggtaaaaga tggccttatt gtgaagtaag agggcatgg gagggcaagg cataactcct      300
tttaaatttt atggactctt taccaggac cccctgtgtt ctcatcagta aggggaaagc      360
aggctctctg gtaagggaaa caagaataaa taggaacttt cataaaaaag caattttaga      420
tattcttttt ataggttttg gcaaagggtg ataaaaggcc tatggaatta ctgctgggtg      480
ctgcacttac atattttgaa tgtcttgaga tgcattgttc tcagtgtatt taattttcct      540
atcttcttta aattctgact cttgacacat actgaaagac cccacctgta ggtttggcaa      600
gctagctgag gatogtttcg catgattgaa caagatggat tgcacgctgg ttctccggcc      660
gcttgggtgg agaggctatt cggctatgac tgggcacaca gacantcggg tgctctgatg      720
ccgccgtgtt cggctgtcan cncagggcnc ccgntttttt tgnaanaccn nctgnccggg      780
ccctnatgaa ctgnngacaa ggcacccggg ttntnggttg ncnaaanggn gtttnttgc      839

```

&lt;210&gt; 116

&lt;211&gt; 815

&lt;212&gt; DNA

&lt;213&gt; Cercopithecus aethiops

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(815)

&lt;223&gt; n is a, g, c, or t

&lt;400&gt; 116

```

tnggggacca gcttgocant tctacaggtg gggctcttca gtatgtgtca agagtcagaa      60
tttaaagaag ataagaaaat taaatacact gagaacaatg catctcaaga cattcaaaat      120
atgtaagtgc agcaaccagc agtaattcca taggcctttt atcaaccttt gccaaaacct      180
ataaaaagaa tatctaaaat tgctttttta tgaaagtcc. tatttattct tgtttccctt      240
accagagagc ctgctttccc cttactgatg agaacacagg gggctctggg taaagagtcc      300
ataaaattta aaaaggagta tgccttggcc toccatgacc ctcttacttc acaataaggc      360
catcttttac ctggttttaga tttgcagact aggtccatta gatacgttgt cattaaatac      420
ctatactata ccctaataatt tgtaatcttg acagggtatta ttttcatttt atagacagat      480
ctaggaaaat tacatgactt atcggaatcc cttcaaatat cacagagcaa agtcatgatt      540
ttaacttgtg tttgncactc tgaaactcac actggaattn tnggggaaat nntatccgnt      600

```

canaattccc ccnecatgag cgtnanaccc cgaaaaaaga acaangatnt ttttggaaacc 660  
 ntttttttttg ggggnaannng gngnngnaaa aaaaaaccnc cnntncnacg ggggtttgtt 720  
 ggcgganaan aacnccacct tttttccnaa ggaaangntt tnaaaangcg aanaccaaaa 780  
 ntgtcntttt gnnnggccgg gttggncccn cttna 815

<210> 117  
 <211> 792  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(792)  
 <223> n is a, g, c, or t

<400> 117  
 ttggggganc gagcggntaa ctttttcaca cagaaattcc cgacctcaag tgatatatcc 60  
 accttggcct ccaaaagtgc tgggattaca ggcattgagc accgcgcccg gcccttcat 120  
 gcagtttctc tctctcttt cagaatcgag gagtctgcta ttccatcgac atctaaccga 180  
 ctctctctaaa ccagcctgca atccagctg gagaactaca atccaatcag ggattaaatc 240  
 taaattcctc ccatctgatc actgggatcc ctaccattc aactccctc ctctctcaga 300  
 aatgttacca atcccctaaa gcctccaatc acctgttgag ccaccagcca agcgcttact 360  
 aatccctgtc tccaagctc agacactccc tgtaattgat ggacacgcag cattggggagc 420  
 tttcacattg agctcttact ttgaaacttt gaataagaaa agagctgaaa aaagcagatc 480  
 tccaatctc ggtgaaactg tagttaaaact ccaagtagaa taccccaata aatggatang 540  
 aatganaaat ctcatatggg ttatatangc antatttana aattttggaa ttataggntt 600  
 anggatncaa actnnanan tantattcca ttggnntttg gngcncccna ngntaaanaa 660  
 gttnnccnct canaaggaaa nggggngggg nannggctan ncnnaancc annttttggg 720  
 ggnnggnnn aaantttttn ggnccaantt naaanaaann tnntnaaaaa aanggnccn 780  
 tttttnaaaa aa 792

<210> 118  
 <211> 838  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(838)  
 <223> n is a, g, c, or t

<400> 118  
 gggnaaccga gcggntaaca ttttcacaca gaaantcgga aagtaaagcc aatcttagag 60  
 gctgcaggag gtttgggggc agtatctgat tcagacgctg gctaacgttt cacgatcgcg 120  
 ttoccttttt tcttccaact cggtaagtaa aaaggcaaga tgagaaattt acgtgctgaa 180  
 ctttaataaat agttggtgga cgtattgcct tttttttttt ttttttggtta agggatgaca 240  
 catctcgtga ctacagttct tttgaggaat aacttttctg ctagtittcca aatcggcacg 300  
 tgaccaaagt cttttcatag gatttttagcg tcctgataaa aatcaatggg cagaatttga 360  
 ttgcttttta aaaaatgtgt ttgtcctttg gtctctggca ccattgtaat ggaaaatccc 420  
 tacattgcct gtactctcag aagctgtcca gtggagcaaa actagagata aagaaacctg 480  
 gaacgattca gttaggaact ttaagaagc cagccttttag ttttctctt agaagattat 540  
 gcagttatca tgattgcttc tctagaactt cagtgtgtta tttggattcc taaatctaag 600  
 acaatgctgn ggaagtctgg ggcttttagn attttngggg ctgctgnaga aaatcctcgt 660  
 ttatactaca aagtttctnt tttggaactt tnggaattgg gcattttttn nnttattatt 720  
 ngnatgntng antnannggc aaaactnagn naaccctttt nggtttgcct cnanccgggt 780  
 nttaaanaaa ngggaaaaan cctnanttta aanttttttc caaccctttt tntttnt 838

<210> 119  
 <211> 820  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(820)  
 <223> n is a, g, c, or t

<400> 119  
 ttgggganct agcttgccaa ntctacaggt ggggtctttc agtggggggc tgtcctgtag 60  
 gttatagaat gtttagcagc aaaaattaaa aattaaataa caaaaataaa aataaaaaag 120  
 aatgttttagc agcatccctg gcctctaccc actagatgtc agcagcacct cccttgcccc 180  
 caggtgtgaa ccaaaaatgc ctgcagacat tgccaaatat ctcttaggag gacaaaattg 240  
 tcctctcttc cacttgagaa ctattactct aaaattaccc agatctgctt tgaatccccg 300  
 ctccaccoca tcacaacctg ggtcatcttg gaaaacagac tgaaccttcc tatgcccccc 360  
 gcaaatctect caactgtaac atggagctct tgcgaagaa atgctatgaa aattaaatga 420  
 aatgatgtac gtacaggatt tacacgcaca gaatattcac cgcgcagag tgagtgtca 480  
 ataaatgggtc agaaatgagg ggaggctaaa aaaaaataat ttcgagaact caaaaatctt 540

```

atcttttaggc ctccagagta ctgtagtcta gacagaagaa atgggtgaga tagaancaaa 600
agagatgaga gaggttgga aagaagtgat agaactaagg tattattccc ottatctctt 660
aagaaccggg ctgggagtca aagccaatag aggggtctact tagttttgnc tattactcta 720
ctttcaata taacgaaaat tgcccaaacc caaagtntcc aaaaaaaact ttnnnttnan 780
cggggatttc tncncggncn aaaatctaan nccccnctnc 820

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<210> 120
<211> 797
<212> DNA
<213> Cercopithecus aethiops

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<220>
<221> misc_feature
<222> (1)..(797)
<223> n is a, g, c, or t

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<400> 120
ttgggggtgc gagcggntaa cantttcaca cagnaattca gctgatgaat gcagatatga 60
accgatgggt caagagctgt agacatacat acctagttta ccacactgat cttcttagta 120
taaaaaaaca agcgttacta agaaacatct actttcagca aatggacatg accagaatga 180
tacatagaat gatgcaagaa atttcactct accattcatt ttaatcttta cagtaacagg 240
atgattgcta tctcaatctg tcattttacc tttttttttt ttttcagaag ttaaagtgt 300
tccatacaag ttcaacttaa cattgttaag tgcaaagtta acagtgtaca ctttggagat 360
accttttttag gtagaaaatg attttttggt ttctaataag ttttcccaag taatattaaa 420
gaagggtaaa tatgtcattt acttggagaa aacagaaaac catgagaaag tttgggaaaa 480
tgctatattt cagagcttaa tatattgaaa cagtaagtaa gacaggaatt ggctaccttt 540
taagaacggt taaaaaata caaactgann ggaatgcttt tggcaatnaa aatntgacnt 600
gaaacattca atggcnnaac attcaanaan gnttnagana tcnttnectt tancatccaa 660
natngttttg ncgncntctc aaaaaantgt ntnttttaaa aaanttaggg ntaaaanttt 720
ctggnagntt nattaanctt tttttgnncc ctnaaatttt nccnaaagt tcnttnanca 780
aaaaaaaatn cttttttt 797

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<210> 121
<211> 828
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(828)

```



<223> n is a, g, c, or t

<400> 121

```

ttgggggancn gcttgccaan tntacaggtg ggggtctttca ccttcttgcc agaaacataa      60
aatgcgatgg agctacggcg accgctgccg agacaaaatg gcgcccagaa cctggtttag      120
cgcagggccc ttggaaagac cctgccccgc ccccgtagaa gccctgggt gcaattctgg      180
gttcctgttc catgggacac tccgccgcca atcctcgtgc cgaactgctc ttcctgacct      240
ctcaattcac caatcagtgc ccagtcaagc acatccggag tcgtctctac caatcatttc      300
tcaagacttg ctactcaat aaccaactct ccaataacgt tgggtcttcgg aaaaagccaa      360
tcataagtgg aagatgtcct acctgctgtt ttctgcacca atccatgaag tttagagct      420
acatccaatg aggacggcag gtagcgaggt cctatccgaa gctcttcggc gtcataaaca      480
gccaatagga gtctgttag aagcgagtct gctcaacagc ttgttatttg gtggattgtg      540
gcagtaaadc ggggcgagtg gggaaccggg cgcaggaact gcagccgcgg ttgggagtg      600

cgcacttnac ccgcanttgg taggtggggg agaggggaat cngggggatn ctgaatggac      720
aaancggnan cggcagcaan tgntgntgcc cgggtncctg tgcaantnga aacntttggn      780
gtggggaang ggattctagg caangnccc gcnanccna aaaaaggc      828

```

<210> 122

<212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc\_feature

<222> (1)..(842)

<223> n is a, g, c, or t

<400> 122

```

ttggggancc tagcttgcca antctacagg tgggggtcttt caccttcttg ocagaaacat      60
aaaatgcgat ggagctacgg cgaccgtgc cgagacaaaa tggcgccgag aacctggttt      120
agcgcaggcg ccttggaag accctgcccc gccccgtgc aagcccctgg ctgcaattct      180
gggttcctgt tccatgggac actccgccgc caatcctcgt gccgaactgc tcttctgac      240
ccctcaattc accaatcagt gccagtcga gcacatccgg agtcgtctct accaatcatt      300
tctcaagact tgcttactca ataaccaact ctccaataac gttgggtctc ggaaaaagcc      360
aatcataagt ggaagatgtc ctacctgctg tttttcgcac caatccatga agtttcagag      420
ctacatccaa tgaggacggc aggtagcgag gtcctatccg aagctcttcg gcgtcatgaa      480
cagccaatag gaggtcgtgt agaagcgagt ctgctcaaca gcttgttatt tgggtggattg      540
tggcagtaaa tcggggcgag tggggaaccg ggcgcaggaa ctgcagccgc ggttgggagt      600

```

```

ggtgctgccc ggacgggggc ccacggagg -tcagagggga ggaggactct ggagctgaca      660
gcgcgcaactt -caccgcagt tggtaggtgg gggagagggg aatcgggggn annctgaatg      720
gacaaancgg cacgggnagc aantgntgnt gcccnnggggt cccggngcaa ttggaanctt      780
ttggaggtgg gggngangna ttctagccaa ngggcccncn nagcccaaaa aaanggncc      840
nc                                                                           842

```

```

<210> 123
<211> 815
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(815)
<223> n is a, g, c, or t

```

```

<400> 123
ttgggnaacc gagcggntaa cnttttcaca cagaaantcc caggctccat goctgaatag      60
ctgggactac aggcacacag aatcatgccc atctaccttt ttattttttg tagagaagag      120
gtctcactat gatgccagg ttggtctcaa acacctgtac tcaagagatc tcccacctt      180
ggcctcccaa agtgccagct ttacaaatgt gagccactgt ggggtggccat gaactcttcc      240
aatgaacctt tttcaaaaaa atatttcaac tattcaatgt gagccaagga tgtgocagac      300
atttgctaga tgctatgaat aaaatatgac aaagattcag tctttgtccc catggacttt      360
atagtctagt agtagatgag actcataagt aatatctagc caaaaataaa aattactgta      420
ttatgggaga ataagaatat ggtactaatt tcttcagtgc caatgtatat cttttcatgt      480
tcttgttccc tggattctca caacaattga tgaaaaatgt aacactggat ttgagtttgt      540
agtcttattt tccaacatga tgaagttggt attaagtgtg agatgatcaa gggagactca      600
ggaagcagtg ggtaacctca gctaaaagca aacagatagt atattggaag atgaggtaaa      660
caaagagagc aaagctttat gaatctgggc taaaantcag ctataagtnt tcgcanatcc      720
angagaactt tncaacagnt tncaattgaa anccttnag tttttaaann cctnttttn      780
caaantgncn aaannnttaa caggnttgna atncc                                815

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<210> 124
<211> 823
<212> DNA
<213> Cercopithecus aethiops

```

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<220>
<221> misc_feature

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&lt;222&gt; (1)..(823)

&lt;223&gt; n is a, g, c, or t

&lt;400&gt; 124

```

ggnnntgcga gcggntaaca atttcacaca gaattcaaac tccagcttta ctaccctgtg      60
accttggggca ggtcacttca catttctcag gctgggttcc agtctggctg cctttgggga      120
ggggacctgg gtttcagga agaaaacttc cttacactga ataattattg ccttgtaga      180
aattttttac catgtgcaca tattactttt cctaaatatt tgcacccaat ttaattgatt      240
taattgggga aaaatgaaca taggaaaaat aatgacctct tcctcagggt tattaaaagg      300
tttcaaaata aagtatgtag ctagtaaagg tgcatagtat atgcttaatc aatagagtgg      360
tgacaggggtg gagggagggt ggaggcaggc tcattcctgc cctggggccc agaggagaac      420
atgtggtaca gaagtccag cctacagcca gctcctagca ttaaggcagg tgccattca      480
gctagagcct canggggggtg cnagttgagg gagctgctcc tancctggnc cccatgccct      540
ttncctttgtg gtggancctt aagaageccn ttttctgan naannoctgg gnttananaa      600
ttcacctttg ncaattacca agnncccggn gnaattntcc ntnttggng aaaaccnttn      660
nntttaaggg tgnntnttng ggattngnac cnnnnttttg gggcncnccc ngntttttn      720
ttttntttnn aaannccnnn aaaanaaaaa aaaaanntnn gngnccnnaa annccccnn      780
ggggggggaa aaaaaaaaaa antttttccc cccccccnc -cnc      823

```

&lt;210&gt; 125

&lt;211&gt; 691

&lt;212&gt; DNA

&lt;213&gt; Cercopithecus aethiops

&lt;400&gt; 125

```

cctaattccac caacccccaa ctactatagt gggagcctga ggtcacagca tggccccccc      60
gtgttgtgag aaaaatctcc acaggattct cccactgtt cctaagtgtg ctctgggatc      120
ctccgtgact agtgtggaat tttagccag tgatttctcc ccacaggttt caattaaatc      180
atctgtcaaa tgaggatgac cacatcttct ttacctacc actgagctgt gaaatgaacc      240
agaggcctta ccttttccc ctgaactccc agtcatccct ggaacacca tttgaacatc      300
atctcccact tcccagcca gttagcagct ctgtcctctg gatttcaaag agaatgtct      360
ctagcatcat ccctgttcc ttgactgtc ctactttctt tttccccca gagccaggaa      420
tgtcttaaac agaatgagat gtcaccaagg ggcaccaac tcacaattag gattcaata      480
aatactgact taagagtga tgaacgatcc ccgtgtctt gtccacattt gtacatgctt      540
acatgattct gcaaagaatc taaatttctc ttacattaa caaacaaggg ggctgggcat      600
gggtggctcat gactgtaatc tcagcatttt tgtaaccag gacagtcctg atgaaataac      660
tgggaaagtt cctttttggg ggggggggtg g      691

```

<210> 126  
 <211> 748  
 <212> DNA  
 <213> Cercopithecus aethiops

<400> 126  
 ccacgcctt actattgctt tcttgacgag ttcttctgag cgggactctg gggttcgaaa 60  
 tgagctagcc cttaagtaac gccattttgc aaggcatgga aaaatacata actgagaata 120  
 gaaaagttca gatcgaggtc aggaacagat ggaacagggc cgaccggctg accggctcgac 180  
 cctagagaac catcagatgt ttocagggcg cccaaggac ctgaaatgac cctgtgcctt 240  
 atttgaacta accaatcagt tcgcttctcg cttctgttcg cgcgcttctg ctocccgagc 300  
 tcaataaaag agcccacaac ccctcactcg gggcgccagt cctccgattg actgagtcgc 360  
 ccgggtaccc gtgtatccaa taaaccctct tgcagttgca tccgacttgt ggtctcgtg 420  
 ttccttggga gggctctctc tgagtgattg actaccgctc agcgggggtc tttcagcagg 480  
 gcccggggcc acagaaggaa aacatctctg tggaatgtgg aaatgcagaa ctctactggg 540  
 cccgtttaga aagcacagaa aagcatggaa gaaagggaga ggcgagaagc ctgaaaaatt 600  
 accctagatc ttaggtatgg atatatcgac ctaaaagaaa gaagatgggg caaagttaat 660  
 gcaagcagag agtttatctg gggtaagct tgaggattgc accccaggag catagattca 720  
 agttgccctg aatttacact gattagca 748

<210> 127  
 <211> 708  
 <212> DNA  
 <213> Cercopithecus aethiops

<400> 127  
 gccaaaccta cagggggggg tcttttactg ccagtcagcg aaccgcgaag ccggcaggca 60  
 cttcggcggt ctccagcctt tgctgaaaa gagctcggca agctagctag aggtcagacc 120  
 ccaggaccca gtcgttttag ctccaggaaa ggaagcgccg gacgccagcc tgcaagcttc 180  
 actgcgcagc cgtggacacc gcccacgctc gtagggccgt ggaccctgac aacgccggaa 240  
 cccggcgctc ggtgcgtgag cttggcggac cagaatggct aacgtaccgc catgccgca 300  
 ggcccacgta gaggcggaag ttgatgggac ggacgcagat gggggaacct tgcctcgatg 360  
 gcactttcct gtccgcgact ccgccccgcg cagaggggct aggtccggg tttcaagatg 420  
 gaggcgctga gtcgagctgg gcaggagatg agcctggcgg ccctgaagca acacgacct 480  
 tacatcacca gcacgcaga cctcacgggc cagggtgctc tgtacacct ctgccccaa 540  
 gccaaaccagt ggggtgagtgc cgcctggctc tgaggacggc cgcggggccg ctgcgggtctc 600

ttaaaggggc cgtgcgtgtt gctgtggggg gggggacaca gcaagagcca gggaggtgaa 660  
gacggggcca gggactgccg agaagccgac cagaaccaga ggggttgt 708

<210> 128  
<211> 741  
<212> DNA  
<213> Cercopithecus aethiops

<220>  
<221> misc\_feature  
<222> (1)..(741)  
<223> n is a, g, c or t

<400> 128  
taacaatttt cacacagaaa ttcaatccaa caaacaanta catattattt tctaagttgt 60  
aaagcctgta accgaatgag ttaattagga aggggtcaatt acaagaaagt gggaaattat 120  
gctagttgtt tttaaacaac taacaaagct tcaagcaggg gctaacgaga atcagtgaac 180  
agactgaatg taacttttcg gaccctctcc agtgcacgaa aagccagaaa gtactgagtc 240  
tgaggggaac attcagagat gacatcacca gcatcatagg tggaaacaaaa cacatttaca 300  
gggtctctct tgtttgtaca aaggctcttcg gggatctagt gaacatggaa gcccttttcc 360  
taagtgcctt gaaatctttt ccgaaactgt gtagttcgat taaagccgga cccaccgcac 420  
tcccccttcc aagaatcgaa actaattgga ttttaagctt taaatccaaa tgacctctga 480  
gaaaggggct ctcatttacg tctgccgggg gagaggagga gtgtttattt tatagacaat 540  
gtatatgcaa tttatctaataatccgcaaa gcctcaaaca caagctttca ggcactcttt 600  
tgacccccacc ggtctcataa cteccaatgt atctgcaaag aaggcaggtc gccacgctcc 660  
ccaaaccoga cgccaaggga ctgatcctgc tccaatcttc cctcactggc ttttccttgg 720  
ggatgtgtnc agcccacttc t 741

<210> 129  
<211> 694  
<212> DNA  
<213> Cercopithecus aethiops

<220>  
<221> misc\_feature  
<222> (1)..(694)  
<223> n is a, g, c or t

<400> 129  
ccgccaacct acaggggtggg gttctttcac tgccagtaca gcgaatccgcg aagccggcag 60  
gcacttcggc ggtctccagc ctttgctga aaagagctcg gcaagctagc tagaggtcag 120  
accccaggac ccagtcgttt tagctcaggg aaaggaagcg ccggacgcca gcctgcaagc 180

ttcaactgcgc agccgtggac accgccocac gtcgtagggc cgtggaccct gacaacgccg 240  
 gaadccggcg tccggtgcgt gcgcttggcg gaccagaatg gctaacgtac cggcatgccc 300  
 cgaggcccac gtagaggcgg aagttgatgg gacggacgca gatgggggaa ccttgccctg 360  
 atggcacttt cctgtccgcg actccgcccc cgccagaggg gctaggetcc ggggttcaag 420  
 atggaggcgc tgagtcgagc tgggcaggag atgagcctgg cggccctgaa gcaacacgac 480  
 ccttacatca ccagcatcgc agacctcacg ggccagggtg ctctgtacac cttctgcccc 540  
 aaggccaacc agtgggtgag tgccgcctgg ctctgaggac ggcgcgtccg gccgctgcgg 600  
 tctcttaaag gggccgtgcg tgttgctgtg ggggtgggga cacagcaaga ggccagggga 660  
 ggtgaagacg gggccaaggg actgncgaaa agcc 694

<210> 130  
 <211> 678  
 <212> DNA  
 <213> Cercopithecus aethiops

<400> 130  
 ccctttactg ccagacagcg aaccgcgaag ccggcaggta cttcggcggg ctccagcctt 60  
 tgccgaaaa gagctcgga agctagctag aggtcagacc ccaggacca gtcgttttag 120  
 ctcaggaaaa ggaagcgccg gacgtcagcc tgcaagcttc actgcgcagc cgtggacacc 180  
 gccccacgtc gtagggccgt ggacctgac aacgccggaa cccggcgtcc ggtgcgtgcg 240  
 cttggcggac cagaatggct aacgtaccgc catgcccga ggcccacgta gaggcggaag 300  
 ttgatgggac ggacgcagat gggggaacct tgcctcgatg gcactttcct gtccgcgact 360  
 ccgccccgc cagaggggct aggtccggg tttcaagatg gaggcgctga gtcgagctgg 420  
 gcaggagatg agcctggcgg ccctgaagca acacgacctt tacatcacca gcatcgaga 480  
 cctcacgggc caggttgctc tgtacacctt ctgccccaaag gccaaccagt gggtagtgc 540  
 cgcttggtc tgaggacggc cggccggccg ctgcggtctc ttaaaggggc cgtgcgtggt 600  
 gctgtggggt gggggacaca gcaagaggcc agggaagttg aagacggggc caagggaact 660  
 ggccgaaaag ccaagcca 678

<210> 131  
 <211> 712  
 <212> DNA  
 <213> Cercopithecus aethiops

<400> 131  
 cccgcagcc tacagggtgg gtctttcact gccagtacag cgaaccgga agccggcagg 60  
 cacttcggac ggtctccage ctttgctga aaagagctcg gcaagctagc tagaggctag 120

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accaccaggac ccagtcgttt tagctcaggg aaaggaagcg ccggacgcca gcctgcaagc      180
ttcactgcgc agccgtggac accgcccac gtcgtcgggc cgtggaccct gacaacgccg      240
gaaccggcg tccggtgcgt gcgcttgccg gaccagaatg gctaacgtac cgccatgccg      300
cgaggcccac gtagaggcgg aagttgatgg gacggacgca gatgggggaa ccttgccctg      360
atggcacttt cctgtccgcg actccgccc cgccagaggg gctaggctcc gggtttcaag      420
ttggaggcgc tgagtcgagc tgggcaggag atgagcctgg cggccctgaa gcaacacgac      480
ccttacatca ccagcatcgc agacctcac ggcagggtg ctctgtacac cttctgcccc      540
aaggccaacc cagtgggtga gtgccgcctg gctctgagga cagccgcccg gccgctgcgg      600
tctcttaaag gggcccgctc gtgttgctgt gggggtgggg gaacacagca agaggccagg      660
ggaggtgaag accggggcca gggacctggc gaaaagcccg aaccagaagc cc              712

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<210> 132
<211> 738
<212> DNA
<213> Cercopithecus aethiops

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<220>
<221> misc_feature
<222> (1)..(738)
<223> n is a, g, c or t

```

```

<400> 132
gccagcctac aggggggggt ctntcactgc acagtacagc gaaccgcgaa gccggcaggc      60
acttcggcgg tctccagcct ttgcctgaaa agagctcggc aagctagcta gaggtcagac      120
cccaggaccc agtcgtttta gctcagggaag aggaagcgcc ggacgccagc ctgcaagctt      180
cactgcgcag ccgtggacac cgccccacgt cgtagggccg tggaccctga caacgccgga      240
accggcgctc cgggtgcgtg gcttggcgga ccagaatggc taacgtaccg ccatgccgcg      300
aggcccacgt agaggcggaa gttgatggga cggacgcaga tgggggaacc ttgcctcgat      360
ggcactttcc tgtccgcgac tccgcccccg ccagaggggc taggctccgg gtttcaagat      420
ggaggcgctg agtcgagctg ggcaggagat gacgctggcg gccctgaagc aacacgaacc      480
ttacatcacc agcatcgcag acctcacggg ccagggttgc ctgtacacct tctgccccaa      540
ggccaaccag tgggtgagtg ccgcctggct ctgaggacgg ccgccggcc gctgcgggtct      600
cttaaagggg ccgtgcgtgt ttgctgtggg gtgggggaca cagcaagagg ccaggggagg      660
gaagacnggg gccagggnac tggcgaagag ccgagccaaa gccagagggg tgtcgggtcc      720
acctgggaat tgggggaa              738

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```

<210> 133
<211> 757

```

&lt;212&gt; DNA

&lt;213&gt; Cercopithecus aethiops

&lt;400&gt; 133

```

cgccaaacct acaggggggg tctttcactg ccagacagcg aaccgcgaag ccggcaggca      60
cttcggcggt ctccagcctt tgcctgaaaa gagctcggca agctagctag aggtcagacc      120
ccaggaccca gtcgttttag ctcagggaaa ggaagcgccg gacgccagcc tgcaagcttc      180
actgcgcagc cgtggacacc gccccacgtc gtagggccgt ggacctgac aacgcggaa      240
cccggcgtcc ggtgcgtgcg cttggcggac cagaatggct aacgtaccgc catgccgcga      300
ggcccacgta gaggcggaag ttgatgggac ggacgcagat gggggaacct tgcctcgatg      360
gcactttcct gtccgcgact ccgccccgcg cagaggggct aggtccggg tttcaagatg      420
gaggcgctga gtcgagctgg gcaggagatg agcctggcgg ccctgaagca acacgacct      480
tacatcacca gcatcgcaga cctcacgggc caggttgctc tgtacacctt ctgcccacag      540
gccaaaccagt gggtagtgct cgctggctc tgaggacggc cggccggccg ctgcgggtctc      600
ttaaaggggc cgtgcgtggt gctgtggggt gggggacaca gcaagaggcc aggggaggtg      660
aagacggggg ccaggggact ggcgaagagc ccgagccaga gccagagggg tgtcgggtcc      720
acctgggatt ggggggatag gaagtgagaa gaagtgg      757

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&lt;210&gt; 134

&lt;211&gt; 668

&lt;212&gt; DNA

&lt;213&gt; Cercopithecus aethiops

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(668)

&lt;223&gt; n is a, g, c or t

&lt;400&gt; 134

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ccagcctaca gggggggggt ctttcactgc cagtacagcg aaccgcgaag ccggcaggca      60
cttcggcggt ctccagcctt tgcctgaaaa gagctcggca agctagctag aggtcagacc      120
ccaggaccca gtcgttttag ctcagggaaa ggaagcgccg gacgccagcc tgcaagcttc      180
actgcgcagc cgtggacacc gccccacgta gtagggccgt ggacctgac aacgcggaa      240
cccggcgtcc ggtgcgtgcg cttggcggac cagaatggct aacgtaccgc catgccgtga      300
ggcccacgta gaggcggaag ttgatgggac ggacgcagat gggggaacct tgcctcgatg      360
gcactttcct gtccgcgact ccgccccgcg cagaggggct aggtccggg tttcaagatg      420
gaggcgctga gtcgagctgg gcaggagatg agcctggcgg ccctgaagca acacgacct      480
tacatcacca gcatcgcaga cctcacgggc caggttgctc tgtacacctt ctgcccacag      540

```



gccaaaccagt gggtagtgatgc cgcctggctc tgaggacggc ccgcccggcc gctgncggtc 600  
 ntcttaaaag gggcccganc gtgtttgctg tgggggtggg gggacncaag caagaaggcn 660  
 cagggagg 668

<210> 135  
 <211> 752  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(752)  
 <223> n is a, g, c or t

<400> 135  
 gcttgccaaa cctacagggg gggcttttca ctgccagaca gccaaccgag aagccggcag 60  
 gcacttcggc ggtctccagc ctttgctga aaagagctcg gcaagctagc tagaggtagc 120  
 accccaggac ccagtcgttt tagctcaggg aaaggaagcg ccggacgcca gcctgcaagc 180  
 ttcactgcgc agccgtggac accgcccac gtcgtagggc cgtggacct gacaacgccc 240  
 gaacccggcg tccgggtgct gcgcttggcg gaccagaatg gctaacgtac cggcatgccg 300  
 cgaggccac gtagaggcgg aagttgatgg gacggacgca gatgggggaa ccttgccctg 360  
 atggcacttt cctgtccgag actccgcccc cgccagaggg gctagggctcc gggtttcaag 420  
 atggaggcgc tgagtcgagc tgggcaggag atgagcctgg cggccctgaa gcaacacgac 480  
 ccttacatca ccagcatcgc agacctcacg ggccaggttg ctctgtacac cttctgcccc 540  
 aaggccaacc agtgggtgag tgccgcctgg ctctgaggac ggccgcccgg ccgctgaggc 600  
 ctcttaaagg ggccgtgctg gttgctgtgg ggtgggggac acagccagga ggccaaggga 660  
 ggtgaagacn ggggcccagg actggcgaag agccgagcca ganccagagg ggtgtcgggt 720  
 tcacctggga ttgggggata ggagttagag aa 752

<210> 136  
 <211> 739  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(739)  
 <223> n is a, g, c or t

<400> 136  
 ctttactgc cagnacagcg aaccgcaag ccggcaggca cttcggcggt ctccagcctt 60  
 tgcctgaaaa gagctcggca agctagctag aggtcagacc ccaggaccca gtcgttttag 120

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ctcagggaaa ggaagcgccg gacgccagcc tgcaagcttc actgcgagc cgtggacacc 180
gccccacgtc gtagggccgt ggacctgac aacgccgaa cccggcgcc ggtgcgtgcg 240
cttggcggac cagaatggct aacgtaccgc catgccgcga ggcccacgta gaggcggaag 300
ttgatgggac ggacgcagat gggggaacct tgcctcgatg gcactttcct gtccgcgact 360
ccgccccgc cagaggggct aggtccggg tttcaagatg gaggcgctga gtcgagctgg 420
gcaggagatg agcctggcg ccctgaagca acacgacct tacatcaoca gcatcgaga 480
cctcacgggc caggttgctc tgtacacct ctgccccaaag gccaaccagt gggtgagtgc 540
cgcttgctc tgaggacggc cggccggccg ctgcggtctc ttaaagggc cgtgcgtggt 600
gctgtggggt gggggacaca gcaagaggcc agggaggtga agacggggcc agggactggc 660
gaagagccga gccagagcca gaggggtgct ggggtccacct gggattggg gataggggtg 720
agagaagnng ctgganaat 739

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<210> 137
<211> 707
<212> DNA
<213> Cercopithecus aethiops

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<220>
<221> misc_feature
<222> (1)..(707)
<223> n is a, g, c or t

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<400> 137
gccaaaccta caggtgggat ctttactgc cagacagcga accggaagc cggcaggcac 60
ttcggcggtc tccagccttt gcctgaaaag agctcggcaa gctagnntag aggtcagacc 120
ccaggaccca gtcgttttag ctacgggaaa ggaagcgccg gacgccagcc tgcaagcttc 180
actgcgagc cgtggacacc gccccacgtc gtagggccgt ggacctgac aacgccgaa 240
cccggcgcc ggtgcgtgcg cttggcggac cagaatggct aacgtaccgc catgccgcga 300
ggcccacgta gaggcggaag ttgatgggac ggacgcagat gggggaacct tgcctcgatg 360
gcactttcct gtccgcgact ccgccccgc cagaggggct aggtccggg tttcaagatg 420
gaggcgctga gtcgagctgg gcaggagatg agcctggcg ccctgaagca acacgacct 480
tacatcacca gcatcgaga cctcacgggc caggttgctc tgtacacct ctgccccaaag 540
gccaaccagt gggtgagtgc cgcttgctc tgaggacggc cggccggccg ctgcggtctc 600
ttaaagggc cgtgcgtggt gctgtggggt gggggacaca gcaagaggcc agggaggtga 660
agacggggcc agggactggc gaagagccga gccagagcca gaggggt 707

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<210> 138  
 <211> 818  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(818)  
 <223> n is a, g, c or t

<400> 138  
 tcacacagaa ttcagaaag cacagctgtc taggcgttg gctcctgaca aatgggtgcc 60  
 tgcctctcac ctcaccagcc tctccagaca cctctgcatc acacagcact gatgaccgcc 120  
 tcccagocca acacccaactc tgcttactct gtgcgccag gctctgattg tgtttgggag 180  
 gtaaagtgtc cagccccaag actggccaaa cttggccctc atcatcccat tctccttgc 240  
 cagtggttta tctaggaata gatatggggc cctgttcagg tcagtgaat gtaaggggtga 300  
 gttagttcag gaatttctga gaaagattct cctctgtaat aaagcagaga gtcacatgac 360  
 tagaaaatct ttttgttggt gtgtgtgtt taccaccacc ccttccttcc tgctttggaa 420  
 atcggtttat gatgtgatgc ctggagctgt ggcagctgtt ttatgaccat gagagaaggc 480  
 ttctccagtg tgctaggatt caggggagga aatacagaat gaatgtcagc cctogatgac 540  
 actgccgagc cctaaaccaa ctctgagaat ttaagacttt ttgttctgta agaaatgaga 600  
 tttatttatt gttaagact ctgttgggta ttctgttatc tgtggccan aatatttta 660  
 ataataat ttctttttgc aataatacat ctcatgga cattccocaa agtctaagac 720  
 tttgagagaa gtcattctctg aagagccaag cattcataat tagaaacttg gccagggtgca 780  
 gtggctcacg cctgtgatcc cagcactttg ggaggcca 818

<210> 139  
 <211> 581  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(581)  
 <223> n is a, g, c or t

<400> 139  
 cacacaaatt agnncaggct atcctcctgg tggctcctgt accagtcctc gatcacctcc 60  
 tcaaactctt ccaccagcac gtcgactgt taatcgtaac acctcacgtt ggcaaagccc 120  
 cagcacctta ctactccta gaggagctca gctaagcctt gcaaccact gcaaggtagt 180  
 .ggcagtggtt cacctaagga aactgaggct agagaggtga aatgacgtga ccaaagccac 240

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cctggcctgg gtggccctcc tcagagcaga cccaateccc accggccctt cactgggcac      300
agcaaccctt ccaagggctg aagggcctgt acctgttctt tgaggtcagc cacctctgca      360
gaagtctcgt tccacagctc ataggggatg tccatcacca ccttgacccc tttgtgtacc      420
aggttgtgta atgtctcaaa ggtctctgac atgccctgga agaagcgacc agacatggga      480
ggcagagctc ccttctctcc ctctaccctt cctctcccag tggggcctat gaactcagct      540
gtaagaccaa tgcccaatgc cctctgagga tcttcaaacc t                                581

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<210> 140  
 <211> 630  
 <212> DNA  
 <213> Cercopithecus aethiops

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<400> 140
tcacacagaa ttocatgttc agtaaccagg tgctacaaat gcagttcaag gctctaggtc      60
atgacaatgt cacagatata tcaggctcag tcaccaaggc aacatgtggc ttgggtcttt      120
ttctggtttc aagactgcat ctgtattctc tcacctccct gggcccacag attocctaaa      180
tcatagcttg gtctaagagc aatgcttcaa attcaggctc cttgtctcag gtgggtagac      240
ttctgtcac ccagccaccg ccacctgatt ctggacctgg agccggcagg occgtggctt      300
cagcccgact cactcttttg tattctgttg cttactatca tctttttttt ttttggctct      360
gaactccgca gtgtcatttt ttttttctag ttatccatc tttgccatgt gtttggggaa      420
gaatggcaat gcgaaagtgt gaacttcag tcccggtta ttagaagccc acagctgttt      480
taaaaaaaat ctacctgtct atcctttccc tttctgtgta cacacaagt actgttaatt      540
agtacctagg ccatgggctg tcatgcttaa aaactgaatg gaattttttg ttcttttagc      600
aatgttagga tgactggctg attataaaaa                                630

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<210> 141  
 <211> 737  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(737)  
 <223> n is a, g, c or t

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<400> 141
acacagaatt cttacttaat acatataaac agaacatttc taggtcagtg acaaaaaata      60
taacctgaat cataaaaaa gagttataac tcttccatca atttccagac atcagccagt      120
ttacaaatcc agaaccctt aaatgaagaa caagcttgat gcccttgagg aagggcccta      180
gtacactgcc caaaatctgt acatttaatt ttcttcttaa tcttccaaa agggacatat      240

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gtccttttac cagtgaact gtcatttgg gtaattgaaa ataatcaaat caggtactac 300  
 tggaccttg ctacgaactg atgcaaattc caggagacct aacatgccat ggtgggccac 360  
 aaagacagt cttatgggaa tcaggtgatc catggagttt taagttgggt ocaactcaca 420  
 tttgaataaa tataactcatg ctgacagaat ctccataatg gttccctgac ctgtaaagt 540  
 aggtgcatta tgggtgggtaa tggcaaatgg aagccagtag aaacacctct atctaggaaa 600  
 aatagtaaag caaatgcaat attttcatct ccgtagggat tgcagacatt agttgccacc 660  
 atcaagggtc tgaaaaatga ccaggggggtg attcccacca acattctnca ttcagctttg 720  
 tctattnggg ccttgcc 737

<210> 142  
 <211> 768  
 <212> DNA  
 <213> Cercopithecus aethiops

<400> 142  
 tttcacacag aattcagtgg atgctatgaa acatatcttc actgttcgtg tttgtctctt 60  
 tctgaatcca caagtgatgg acacatgaat ctactactac tgttctcttt tcttcttttt 120  
 ccgtctttct ctcccttccc acccctagtt cctgacgttt gctactcta tcatgtctgc 180  
 agtgttgcac accactctgc atcctcatct gtctgagaca cattcaacca ctaggtcttc 300  
 agctgcttca ctgctgcctg atgttctttg aagtcagta taagagagaa cattctattt 360  
 tgctaaaact aaaagactac cctttatctt tgctgagaat atgtaaagaa aaggggaatg 420  
 actagatcag aaggcttatt ctgaggtata tagtaatgtt aattttttaa taattgttag 480  
 gtgttcttct tcattaggta ttcaccttca gttttccaag actatggaaa gcaccattgg 540  
 tgcagttagt taacagcagc ttgactcaga cgtagaactg cagccaggac ocatctgttc 600  
 cccattactc cctgctgcca gttttgcaac cagaacctag gagtgattta tccatcctc 660  
 aattttgctc aggactcagc agaagaagga tcttgggaca caagactttt cagtggcttc 720  
 aaacttggga gagttctttg gcaatgcaca ggtttgacct atgaactg 768

<210> 143  
 <211> 450  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(450)  
 <223> n is a, g, c or t

<400> 143  
 gcctgtgaaa ccactctggnc ctggactttt ttgggttggg aggctatcaa cttattgcct 60  
 caatttcaga gcctactatt ggtctattca gggatctcaa ctncctcctg gctttagtct 120  
 tggaagagtg taagtgtcca ggaaatctat ccactctctt ctagattttc cagtttattn 180  
 cgcgagagg cggtcacagc agcctctgat ggtagttcga atttctgagg ggcggcggn 240  
 gatatocctt ttatcatntt naatngcgnc gatnagacnc ttctctcttn tcttctttat 300  
 aagcactcng ctagecggcc ngccaatntc gnnngangctt ntcaaaaaac caactcctgg 360  
 attcatcgat tncnntggag ggtctntttg ngtctctatc tccttcagtn actgcntga 420  
 tcttagnata tttcntgcn tctgctagct 450

<210> 144  
 <211> 729  
 <212> DNA  
 <213> Cercopithecus aethiops

<221> misc\_feature  
 <222> (1)..(729)  
 <223> n is a, g, c or t

<400> 144  
 cacacagaat taoccttttc gccttccaag gggaaaccag gccactttgc tcttcttggg 60  
 gaaggaggat aattgtccag tgctgggagg tgacagcagc tactgccagc acgagggtggg 120  
 gccctgcag tgtggttcct caggctctgag aggggttccc tctgccttcc tccctcctgc 180  
 tcccttttcc tcttctctct acctgttttt tcttctctc acatctctcc tgcttccca 240  
 caatccctga catttactgc aggetcccga agagccatga cactttatac cctcaacctc 300  
 atttaattct caggaaaacc cacaaggccg tgcaattctc accccaggta ccaagtgagc 360  
 cagttcaggt gcacagagac tgccttctgc ccagagatcc tagcacgagg gctctgtact 420  
 ggttagggtc tccagagaaa cagctccaat agaattgtga gatgctgggt gcagtggctc 480  
 acccctgtaa tccagcact ttgggaggcc gaggcgggcg gatcatgagg tcaggagatc 540  
 gagaccatcc tggctaacac ggtgaaacc catctctact aaaaatacaa aaacattagc 600  
 cgggccgtgg tggcgggncg cctgtagtcc cagctacttg ggaggctgag ggcaggagaa 660  
 tggcatgaag ccganaggca nagcttgagc tgagccaaga tcacatggca ctccaacctg 720  
 ggcgacaaa 729

<210> 145  
 <211> 755  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(755)  
 <223> n is a, g, c or t

<400> 145  
 aacaattttc acacagaatt acctggtctc aaagtgtatc ctccatgctt cggcctccca 60  
 aagtattgtg attacaggag tgaccacccc tgcccggccc tctagcttat ggtggaagct 120  
 taaataatca gttttagaca tttcttcttc ctttttttcc caagaaacag ggtcttgctc 180  
 tgccaccac gctggaatga agtggtgcaa tcatagctga ttgcaacctc aaactcctta 240  
 actcaatcaa tctctccacc ttagcctttc aaatagctgg gactacagtg cgtaagccac 300  
 cgcacctggc ctcttctttc taatataagt atttaatat ataaaaattc ctctaagatc 360  
 taaacactgc tttagctgca actcacaat tttgatatgt tgtattttta tttatatccc 420  
 attaaaaata cagtattagt tcccgtgtga tttcttcttt gacctatggc ttagaagtg 480  
 gttgttttagt ttccaaattt gggggcattt tccagatata tttctcttat ttatttgtaa 540  
 tttaattctg ttgtggtcga ggagcacgtt ctgtttgctt acaatcctcg taaatttatt 600  
 atgacttggt ttatggccca gcataggggc tgtttggcga gtgttccatg tgcactgaa 660  
 aagaatgtgt attctgtagt tgtgcagggt atttttaaaa ttttattctt ttcactgana 720  
 caaaatagct gtncatattt agaggggtaca tgcga 755

<210> 146  
 <211> 795  
 <212> DNA  
 <213> Cercopithecus aethiops

<400> 146  
 ctaccagtat atacaaagaa aagctcgtac cattcatgct gaaactactc caaaaagttg 60  
 aggagaagga aatcctccct agcttattct acaaagctag catcacactg ctaccaaaac 120  
 ctgacagagt cacaacaaca aaaatttcag acatatattc ttgatgaaca ttgatgcaaa 180  
 gtagtcaaca aaatacttgc aaaccaaatt cagcagcaca tcaaaaagct tatccatcat 240  
 gatcaagtag gctttatccc tgggatgcaa ggttggttca acatctgcaa atcaataaat 300  
 gtgattcatc acataaatac cactaaagac aaaaaacca catgattatc tcaacagatg 360  
 cgaaaaaggc ttttgataaa atccaatacc ccttcatggt aaaaactctc aataaactag 420  
 gtattgaagg aacatacctc aaagtaataa gaaccaccta taaaaaacc acagccaaca 480  
 tcatattgaa tgggcaaaag ctggaagcaa tccccttgaa aactggagga agacaagaat 540  
 accctttctt accactccta ttcaacataa tatttggaagt cctggccagg acaagcaggc 600

aagagaaaga aagaaaggca tcccaatagg aagaaaggga agtcaaacta tocctgtttg 660  
 cagacaaaat gatcctatag ctagaaaccc catagtctca gcccaaagct ttttaagctga 720  
 taaacacttt cagcaagcct cagcatacaa aatcatgtgc aaaagtcagt acatttttga 780  
 caccaccaac agtca 795

<210> 147  
 <211> 704  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(704)  
 <223> n is a, g, c or t

<400> 147  
 gcatcctccc tcctcggcct gggcgtgggc tcgcaaaacg ctgggattcc cgggtattaca 60  
 ggcgggcgcg ccacgccagg agcaaacact tcctgcttta aaaattcagt gttgtgattg 120  
 gctgccattc agcattatgc taattaagca tgcctgtttt ttttaagctt cttaaaacaa 180  
 ttttttaaaa ttocgtttcc acctaaaacg ttaaaatttg tcaagtgata atattcgaga 240  
 agatgttggt gccaaactat ttttctattt gtttcctaata ggcatcggaa atagcgaaag 300  
 tatctcgcca ttagttaaaa gttggcagca gatgtagacc ccgcagaggc tgcgagtggg 360  
 ctgttaagac tatactttca gggatcattt ctatagtttg ttactagaga agttctctct 420  
 gaacgtgtag agcaccgaaa accacgagga agagacgtag cgttttctcc tgagcgtgaa 480  
 gcgggcggtt ggtgttgctt cgctgcaact gccatcagcc attgatgac gttcttctct 540  
 ccgctttgga gagnaagagg gagagaacgc ggtctgagt gtttttcttt ttgcnnggt 600  
 tagaacgaca gactgtacag cgaccgntc ccggcttgnc tntgtgcttg nntgncncc 660  
 ngaggccnaa gngagttgcc ttattttgtt tcagnanccg ntgt 704

<210> 148  
 <211> 650  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(650)  
 <223> n is a, g, c or t

<400> 148  
 atcgcttct atcgcttct tgacgagttc ttctgagcgg gactctgggg ttcgaaatga 60  
 gctagccctt aagtaacgcc attttgcaag gcatggaaaa atacataact gagaatagaa 120



```

aagttcagat cgaggtcagg aacagatgga acagggtcga cgggtcgacc ggtcgacct 180
agagaacctat cagatgtttc caggggtgcc caaggacctg aaatgacctt gtgccttatt 240
tgaactaacc aatcagttcg cttctcgctt ctgttcgcgc gcttctgctc cccgagctca 300
ataaaaagagc ccacaacccc tcaactgggg cgccagtcct ccgattgact gagtcgcccg 360
ggtagccgtg tatccaataa accctcttgc agttgcatcc gacttgtggt ctcgctgttc 420
cttgggaggg tctcctctga gtgattgact acccgtcagc gggggtcttt cagttaagac 480
tatactttca gggatcattt ctatagtttg ttactagaga agtttctctg aacgtgtaga 540
gcaccgaaaa ccacgaggaa gagacgtagc gttttctcct gagcgtgaag cgggcgtttg 600
gtgttgcttc gctgcactgc catcancat tgatgatcgt tttntntccg 650

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<210> 149
<211> 671
<212> DNA
<213> Cercopithecus aethiops

```

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<220>
<221> misc_feature
<222> (1)..(671)
<223> n is a, g, c or t

```

```

<400> 149
aactttaact aatggcgaga taccttcgct attgccgatg ccattaggaa acaaatagaa 60
aaatagtctg gcaacaacat cttctcgaat attatcactc gacaaattat aacgttttag 120
gtggaaacgg aactttaaaa aattgtttta agaagcggaa aaaaaacagg catgcataat 180
tagcataatg ctgaatggca gccaatcaca aactgaatct ccaaagcagg aagtgtttgc 240
tcctggcgtg gcgcgcccgc ctgtaatccg ggaatcccag cgtttagcga gccacgccc 300
aggccgagga gggaggatcc ttgttccac gagatcgaca ccagcctagg caatatagca 360
gaatcctggg ggtgacggaa atgccctatc ttgagcttat caatgccaaa accccgggtca 420
tataacttta ttggatatca gtggggaaaa ctgagtaaaa ggtgcaaatt tataactcag 480
tataaacccc aagaacgaaa cgcaaacctt accattctct gaaagaaatg ttttgtacat 540
atatttacac agaaacacat acatcatgat caaaaaatga catcattcgt aaaaaaaaaat 600
aacaaaaagt gtaaaagaac ccacgcgccg gaaaggaagg gccctgtgag accggatccc 660
caaaaccaa c 671

```

```

<210> 150
<211> 704
<212> DNA
<213> Cercopithecus aethiops

```

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(704)

&lt;223&gt; n is a, g, c or t

&lt;400&gt; 150

```

tcattaacag cccactcgca gcctctgcgg ggtctacatc tgctgccaac ttttaactaa 60
tggcgagata ctttcgctat ttccgatgcc attaggaaac aaatagaaaa atagtttggc 120
aacaacatct tctcgaatat tatcacttga caaattttaa cgtttttaggt ggaaacggaa 180
ttttaaaaaa ttgttttaag aagcttaaaa aaaacaggca tgcttaatta gcataatgct 240
gaatggcagc caatcacaaa ctgaattttt aaagcaggaa gtgtttgctc ctggcgtggc 300
gcgcccgcct gtaatccggg aatccagcg ttttgcgagc ccacgccag gccgaggagg 360
gaggatcctt tgttccacga gttcgacacc agcctaggca atatagcaga attctgtgtg 420
aaattgttat ccgctcacia ttccacacia catgagcgtc agaccccgaa gaaaagatca 480
aaggatcttc ttgagatcct ttttttctgc gcgtaatctg ctgcttgcaa acaaaaaaac 540
caaccgctacc agcgggtggt tgtttgcgg atcaagagct accaactctt tttccgaagg 600
taactggctt cagcagagcg cagataccaa atactgtcct tctagtgtag ccgtagttag 660
gccnccact tcaagaactc tgtagcaccg cctacatacc tcga 704

```

&lt;210&gt; 151

&lt;211&gt; 705

&lt;212&gt; DNA

&lt;213&gt; Cercopithecus aethiops

&lt;400&gt; 151

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gctatattgc ctaggctggt gtcgaactcg tggttaacaaa ggatcctccc tctcggcct 60
gggcgtgggc tcgcaaaacg ctgggattcc cggattacag gcgggcgcgc caccgcagga 120
gcaaacactt cctgttttaa aaattcagtt tgtgattggc tgccattcag cattatgcta 180
attaagcatg cctgtttttt ttaagcttct taaaacaatt ttttaaaatt ccgtttccac 240
ctaaaacggt aaaatttgtc aagtataat attcgagaag atgttgttgc caaactattt 300
ttctatttgt ttctaattgg catcggaat agcgaaagta tctcgccatt agttaaaagt 360
tggcagcaga tgtagacccc gcagaggctg cgagtgggct gttaatgaaa gacccacct 420
gtaggtttgg caagctagct gaggatcgtt tcgcatgatt gaacaagatg gattgcacgc 480
tggttctccg gccgcttggg tggagaggct attcggtat gactgggcac aacagacaat 540
cggtctctct gatgccgccg tgttccggct gtcagcgag gggcgcccg tttttttgt 600
caagaccgac ctgtctggtg ccctgaatga actgcaggac gaggcagcgc ggctatcgtg 660

```

gctggccacg acgggcggtc cttgcgcacc tgtgctcgac gttgt

705

<210> 152  
 <211> 673  
 <212> DNA  
 <213> Cercopithecus aethiops

<400> 152  
 tttcattaac agccactcg cagcctctgc ggggtctaca tctgctgcca acttttaact 60  
 aatggcgaga tactttcgct atttccgatg ccattaggaa acaaatagaa aaatagtttg 120  
 gcaacaacat cttctcgaat attatcactt gacaaat ttt aacgttttag gtggaaacgg 180  
 aattttaaaa aattgtttta agaagcttaa aaaaaacagg catgcttaat tagcataatg 240  
 ctgaatggca gccaatcaca aactgaattt ttaaagcagg aagtgtttgc tcctggcggtg 300  
 gcgcgccccgc ctgtaatccg ggaatcccag cgttttgcga gccacgccc aggccgagga 360  
 gggaggatcc ttgtttccac gagttcgaca ccagcctagg caatatagca gaattcatct 420  
 cacagagtta catctttccc ttcaagaagc ctttcgctaa ggctgttctt gtggaattgg 480  
 caaagggata ttggaagcc catagagggc tatggtgaaa aaggaaatat cttccgttca 540  
 aaactggaaa gaagctttct gagaaactgc tctgtgttcc tctgaattct ggaagaaaac 600  
 aaacacatca ttcttgtctc caagagctta aatttctgtt tgggcaattt atttataaaa 660  
 acacaactta gcc 673

<210> 153  
 <211> 709  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(709)  
 <223> n is a, g, c or t

<400> 153  
 tttcattaac agccactcg cagcctctgc ggggtctaca tctgctgcca acttttaact 60  
 aatggcgaga tactttcgct atttccgatg ccattaggaa acaaatagaa aaatagtttg 120  
 gcaacaacat cttctcgaat attatcactt gacaaat ttt aacgttttag gtggaaacgg 180  
 aattntaaaa aaagttttta agaagcttaa aaaaaacagg catgcttaat tagcataatg 240  
 ctgaatggca gccaatcaca aactgaattt ttaaagcagg aagtgtttgc tcctggcggtg 300  
 gcgcgccccgc ctgtaatccg ggaatcccag cgttttgcga gccacgccc aggccgagga 360  
 gggaggatcc ttgtttccac gagttcgaca ccagcctagg caatatagca gaattctgtg 420  
 tgaaattgtt atccgctcac aattccacac aacatgagcg tcagaccccg aagaaaagat 480

```

caaaggatct tcttgagatc cttttttttc tgcgcgtaat ctgctgcttg caaaacaaaa 540
aaaccaccgc taccagcggg ggtttgtttg cncgggatca agagtctacc aacctctttt 600
ttacgaaagg tnaactgggct tcaggcagga gccgcanatt nccaaaataa ttggnocctt 660
ccaagngggn ancccgcnag gnttagggcc cnoccaactt tcnaaggac 709

```

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<210> 154
<211> 574
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(574)
<223> n is a, g, c or t

```

```

<400> 154
cctcggcctg ggcgtgggct cgcaaaacgc tgggattccc ggattacagg cggggcgcgcc 60
acgccaggag caaacacttc ctgctttaaa aattcagttt gtgattggct gccattcagc 120
attatgctaa tnaagcatgc ctgttttttt taagcttctt aaaacaattt tttaaaattc 180
cgttaccacc taaaacgtta aaatttgtca agtgataata ttcgagaaga tgttggtgcc 240
aaactatttt tctatttgnt tcctaattggc atcggaaaata gcgaaagtat ctcgccatta 300
gttaaaagtt ggcagcagat gtagaccccg cagaggctgc gagtgggctg ttaatgaaag 360
acccacctg taggtttggc aagcatagct gaggatcgtt tcgcatgntt gaacaagatg 420
gattgcaegc tggntctccg gccgctngng tggagaggct attcggnat gactgggcac 480
aacagacaaa tcgggctgnt ctgatgccgc cgtgttccgg ntgtaagcgc aggggcgccc 540
cngtttcttt tttgnaaaga ccganctgta acgg 574

```

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<210> 155
<211> 794
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(794)
<223> n is a, g, c or t

```

```

<400> 155
actccggaga tatgaggcct agtccatcc ttcttttctt atcaactcagt cattcaatct 60
ttgcttgga tacaatgaact aataatttcc aatattacct gacatggatc cactttaggg 120
aagacacaag atatgaaaga aaggataaag tctgaaagtt agaagtaaca caactacaga 180

```

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aatagatta atgtggattg ttatagccat tcatacaatg acatcctcaa cgtcaaaacc 240
tttttgtact ctttacagat tccacatcca agcagaattc tatttaaatgt gctttctaac 300

aatcagattc ctgacaaatg tgttcataaa gtaataaaag cagcaaaatc ttaaattgtt 360
tatactaaca tagtagacaa aatacaata ctctgaacac taatatcaca gaaaccctta 420
aaaaaaagat tgaggggagg taataacata cctaatacaa atagaaataa ggaggaacct 480
ttgaggtttg ctatgctttg aacgtgtccc caagggtcac atgttggaat cttaatccct 540
gaagcaacag tgatgagaag tgggaccttt aagagggtgag taggtcacga gggctctgct 600
ctgccacatg aatggattaa tgctattacc agaggagtgg ggaatgggtt ccagatagaa 660
gaccgagttt ggectectcc ttatntntcg ctctctngcc ttccgecttc taccatggga 720
tgatacagca ggaagacct agataccaca ccttgatatg gacttccngt ccnanaacct 780
tgantaaata ccag 794

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```

<210> 156
<211> 831
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(831)
<223> n is a, g, c or t

```

```

<400> 156
cgcacgcgct tctatgcct tcttgacgag ttctcttgag cgggactctg gggttcgaaa 60
tgagctagcc cttaagtaac gccattttgc aaggcatgga aaaatacata actgagaata 120
gaaaagttca gatcgaggtc aggaacagat ggaacagggc cgaccggctg accggctcgac 180
cctagagaac catcatatgt ttccagggcg cccaaggac ctgaaatgac cctgtgcctt 240
atttgaacta accaatcagt tcgcttctcg cttctgttcg cgcgcttctg ctccccgagc 300
tcaataaaag agcccacaac cctcactcg gggcgccagt cctccgattg actgagtcgc 360
ccgggtaccc gtgtatccaa taaacctctc tgcagttgca tccgacttgt ggtctcgtg 420
ttccttgga gggctctctc tgagtgattg actaccgctc agcggggggtc tttcaaggtc 480
aactgacttt aaacttgccg ttgatttgt gactttagaa agtagagtta actatattta 540
gcaatatgct taagcatgtg catatcacct catgaaacgt gtgtgtgcat gagaaaagct 600
gcctccagta catatacata tgtatataaa cacacatata cacaagcata tatatgtatg 660
tatttcttgn aggaccagtc tcattgtata taatttcaag tgcaggttcc tgatctccan 720
ggatgcgtaa aagactcact gaagttinga agaaanttta nggctactat tntgttgng 780
atcncacct tcaagtttaa atttgatntg attattctta cngnttgng g 831

```

<210> 157  
 <211> 637  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(637)  
 <223> n is a, g, c or t

<400> 157  
 caacctaaga aaaactcaca gccactttta aagcagtaac acatgtataa agtatagttt 60  
 ggatcctttt gtacacagct cctgaaagag agaaattttt ttttcaccta ccgacagaca 120  
 tattggaagg ctgctaatat tctgactttt acggactgta ctccctttaa cctgggtaca 180  
 taccataata ttctttcagt tgnccacagc tatagatacc cctagcataa cacttcagga 240  
 ttcagaagac gaatgtacct ttctgtatct taacctctct actccacact tcccacctct 300  
 gaaaaaacia caggccaaat tctcagaacc taaaaccaag tcagagtaaa cactgctaata 360  
 acaataactga cacttacata tttacctggc ataattctta ggattccacc cacaacctaa 420  
 cagatcctaa ctctctcata gagngagaaa atctgctaaa atctgacaga agtccaaatg 480  
 aatcctttca gatataatgta gcttgctaca cactcagaaa gnaaagttct cggaacttga 540  
 aagctctctg aaactnttac cagntacaag angttncagc nnatcacact agcagcatgg 600  
 ntaanggcaa accagagcag ctaccggaan attaaag 637

<210> 158  
 <211> 656  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(656)  
 <223> n is a, g, c or t

<400> 158  
 tccatacctt taaaattcaa gaatgttgtg ttctaattggc agtttgaccg ttgagatatt 60  
 aacataggaa catcatttag cctcttaagc ttgaacatcc attaaagcggg aaaaatagtg 120  
 cttatttctt agaggtttgc agacattggc taaccaatag ttntgattnt gctggaaagc 180  
 aatgtgcaaa ttttcttaga tgtgatcgct tcattttctc ttacatttta gattggcagc 240  
 agocaaatgg gcgttccagc ccctnatctc ctgcaagatt cttctcagtt tcataaatct 300  
 ggtaattttt gagctctttt cccaacaggg tgctgcagct caccaagtgg aatctacaac 360

attttctgct accaggatag cagcttgcca gcaggatata ctgaaattac tgggttbcag 420  
 tatgatgttg gctggtacga acntcaatca tncgaatcga catgcgcccc gacattctca 480  
 taatgaaatg tntccttctc ctttcaacat gtcccgcttt ccagccccc atcctcctt 540  
 tattatnttt tttctttcan nnaaaagaag ctttnagnaa acacnnaaac ctcttactcc 600  
 ctntagnгаа agggaaaacnt tctttccnnt nctnctcc ctttngannc noccta 656

<210> 159  
 <211> 654  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(654)  
 <223> n is a, 'g, c or t

<400> 159  
 cattttaatt tttatatagg atggtattta tgaacatccc actaactatt ctgccgctga 60  
 ttgatatttg gatgtgtaca gtttgatgct attataaaat tcttctaaga acattcttgt 120  
 acatgttcat tttgtttcgc taggtcctag agtctaaggt atatatccag aagaggaata 180  
 gctgggtatt atgatagaat aatgacaaac tagtttctaa agtgattgta ccaattagtg 240  
 tttccatagg agaaaagtgt acagctactg gaaaaacagt ttggaatgat ctgaagtata 300  
 agaatgttca tagcaacaga atgtgtttct tgtattccaa atgttcacct acagttggtg 360  
 tggtcagtat aagttgttgt tttgtttttt attgtgtgtg tgtttttttt atcctttggg 420  
 acagggcctc actttgttat ccaggctaga gagcagtggt acaaacatga ctactgcag 480  
 ccttagcctc ccaggctcaa gcagtcctcc tgcctcagcc tccctaagta ctgggactac 540  
 aggcattgtc caccacacct ggctaatttt tgtattttnt tgtagagaca gggtttcacc 600  
 atgttngccc agtctggtct agttttaaac aaagttgtng cctgnggaaa tgat 654

<210> 160  
 <211> 683  
 <212> DNA  
 <213> Cercopithecus aethiops

<400> 160  
 ttactgcac tgcacacaaa aaccaccga agaaaaaag tgtgaatgcc atacaatttt 60  
 tttcaatgca agtatggaac actgtacatc actgaaaaac agggggaaaa aaaaaagga 120  
 aaaagaggag aaccattgaa gaaagcataa aatagcagct agctttctta cgtgtgctgg 180  
 aattgtgtct ttcgggttaa ccccaaattt tcctatgcta tacactcttc tcacatttg 240  
 gtcaatacta gcttctgaat tggaagagggc attatcaatt gctttaaaat gttatacct 300

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aaataaagaa acaactgagtt agactgtcac cactttgaat acccatcagg agagtgtggc 360
attgcatgcg aaaatgtatg tgttcctctt aggagatgaa gatcaagtca gctaacagct 420
gtcaacaaac ttctagtgtg ggcaagaatt ttatggccaa gttgggcttt cctttattcc 480
ttactggaag aaagtattca gaaaatagca ttttagggga aaaaagtgtt aagtaaacag 540
aatcctttta agcacacaaa caaaagtga gcagtgtaaa ttttgaaact tagtgccctt 600
tagtatctga agcaaaatga taacaagtta taggattttt tctttatgaa gaatgatgta 660
agctcactta tgaaagaaga acc 683

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<210> 161
<211> 811
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(811)
<223> n is a, g, c or t

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```

<400> ..161
ctttcacgag aattctgtct caaaaaaaaa aaaaagcca aagtcctcaa aatggcctgc 60
atggcactac attctctggc cctttatcag cactctgaca gctctctcct ttgcttattt 120
tgctcctcat tctagcctct ggatctttgc ccttgctgtt ccttacgctc ttctccagg 180
gatctgaaag gctcacacc tcacctcctt cagagggttg ctaaaatgtc ttctaccag 240
tgaagccttc cccaaccacc acattaaaaa cacacaacca gcaccggtc tctatcttcc 300
ttcactttgc atttgccat tgtgtaacat cacttacata cctttaattt ttagtttatt 360
aatccatact gcaaaacaac ttagtttnta ccatgtgcc ggcattgtcc ctagttgctg 420
acaatacagt tgaaaataaa atagacaaaa atcccatctt ttgaatcttt tgaaccttac 480
attgggagtg acaggcaaaa acgaggtaaa tcagtaaaat acgtgagaca gaacgctaaa 540
agaaaaaaaa gaggaagggt ctgatttttg tgtctttccc tccanaatgc aagctccctt 600
gaggatacag atttgngtgt tttttaacta ctgnaatnct ccctgacaat agcgccccag 660
tnacatagta agggcatttc gannccaatt ttttaaaaat gaagaaaact agggcagtta 720
ccncagtttc ctggggccca attttcaact ttttagganc ntnaantacc gatataaana 780
aaattcggtt acagctaggg ctccgnatna a 811

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```

<210> 162
<211> 757
<212> DNA
<213> Cercopithecus aethiops

```



<220>  
 <221> misc\_feature  
 <222> (1)..(757)  
 <223> n is a, g, c or t

<400> 162  
 ctttcacgag aattctgtct caaaaaaaaa aaaaaagcca aagtcctcaa aatggcctgc 60  
 atggcactac attctctggc cctttatcag cactctgaca gctctctcct ttgcttattt 120  
 tgctctcat tctagcctct ggatctttgc ccttgctggt ccttacgctc ttctcccagg 180  
 gatctgaaag gctcacaccc tcacctcctt cagagggttg ctaaaatgtc ttctaccag 240  
 tgaagccttc cccaaccacc acattaaaaa cacacaacca gcaccggtc tctatcttcc 300  
 ttcactttgc atttgccat tgtgtaacat cacttacata cctttaattt ttagtttatt 360  
 aattcatact gcaaaacaac ttagttttta ccatgtgcc ggcattgtcc ctagttgctg 420  
 acaatacagt tgaaaataaa atagacaaaa atcccatctt ttgaatcttt tgaaccttac 480  
 attgggagtg acaggcaaaa acgaggtaaa tcagtaaaat acgtgagaca gaacgctaaa 540  
 agaaaaaaaa gaggaagggt ctgatttttg tgtcttcctt ccagaatgca agctccttga 600  
 taggcattcg atccaatttt aaaatgagat actaggcagt tactcagttt tctgggcaca 720  
 tttcaacttt tagacaataa taccgataag aaaanta 757

<210> 163  
 <211> 749  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <222> (1)..(749)  
 <223> n is a, g, c or t

<400> 163  
 ctttcacgag aattctgtct caaaaaaaaa aaaaaagcca aagtcctcaa aatggcctgc 60  
 atggcactac attctctggc cctttatcag cactctgaca gctctctcct ttgcttattt 120  
 tgctctcat tctagcctct ggatctttgc ccttgctggt ccttacgctc ttctcccagg 180  
 gatctgaaag gctcacaccc tcacctcctt cagagggttg ctaaaatgtc ttctaccag 240  
 tgaagccttc cccaaccacc acattaaaaa cacacaacca gcaccggtc tctatcttcc 300  
 ttcactttgc atttgccat tgtgtaacat cacttacata cctttaattt ttagtttatt 360  
 aattcatact gcaaaacaac ttagttttta ccatgtgcc ggcattgtcc ctagttgctg 420  
 acaatacagt tgaaaataaa atagacaaaa atcccatctt ttgaatcttt tgaaccttac 480

```

attgggagtg acaggcaaaa acgaggtaaa tcagtaaaat acgtgagaca gaacgctaaa 540
agaaaaaaaa gaggaaggg ctgatttttg tgtcttcctt ccagaatgca agctccttga 600
ggatacagat ttgggtgttt tntactactg natctcctga acaatagcgc cccagtacnt 660
aggtaggnca ttgatccaa nttttnaaaa agagganccct agggccagtt aactnaagtt 720
ttctggggcc ccatttccaa acttttaga 749

```

```

<210> 164
<211> 741
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(741)
<223> n is a, g, c or t

```

```

<400> 164
ctttcacgag attctgtctc aaaaaaaaaa aaaaagocaa agtcctcaaa atggcctgca 60
tggcactaca ttctctggcc ctttatcagc actctgacag ctctctcctt tgcttatttt 120
gtccttcatt ctagcctctg gatctttgcc cttgctgttc cttacgctct tctoccaggg 180
atctgaaagg ctacacacct cacctccttc agaggtttgc taaaatgtct tctaccaggt 240
gaagccttcc ccaaccacca cattaataaac acacaaccag caccggttct ctatcttctt 300
tcactttgca ttgttcatt gtgtaacatc acttacatac ctttaatttt tagtttabta 360
attcatactg caaaacaact tagtttttac catgtgccag-gcattgtccc tagttgctga 420
caatacagtt gaaaataaaa tagacaaaaa tcccatcttt tgaatctttt gaaccttaca 480
ttgggagtgga caggcaaaaa cgaggtaaat cagtaaaata cgtgagacag aacgctaaaa 540
gaaaaaaaaa gaggaaggg ctgatttttg tgtcttcctt nccagaatgc aagctccttg 600
aggatacaga attngtgtgt tttttnacta ctgnatctcc tgacaatagc ncccagtaca 660
tagtaggcat tcgatccaat tttnaaaaga ganactaggc angtaactaag tttntgggcc 720
cattnnactt ttaagacaat a 741

```

```

<210> 165
<211> 727
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(727)
<223> n is a, g, c or t

```

&lt;400&gt; 165

ctacgataca tgaacattc tacgaacaac catggtgagt agaaccatct ggattttcca 60  
 tcaactttcat ttaaaagact ctgttgatat tctaggtact gattccatat atcagtatca 120  
 acaaatctct caaccaagg gataattggt ttatctgttt gcaattcatt ccgtaattta 180  
 gaaaggagag aaatagcttt cttttcagct tccacgcctt cctgcaaaaa tacaagaaaa 240  
 atcaattgtg tgtgtgtctg tgtctgtgtt tgtgtgtgcg tgtctatgca attcctctag 300  
 ggtaacatat ttttacagac ttaagaagaa aagaaaaatg ttcaaaactac attatacttc 360  
 tttaaacatt acatttagaa ctcttaaact gaaaatcaaa aaacacacac agatctcata 420  
 tgaacataat catgccttat ctatctaagt tctggccttt ctgtgtcttc ggtgatcatt 480  
 actacagagg gaaaggaacc cctgacagat tttccatgtc tttcatgctt ccatacacat 540  
 tcttctttca ccaatgacac cactagaaaa gaaactgtgg cctttctgag gtttcttttg 600  
 gtagctcaat tttttttttt aacttgtttt cactgagtt ctagctaggt gagagatgag 660  
 atatgctgac atacaaggcg ctacaatata tctcacatga caggccantg ggagtgggga 720  
 naaatgt 727

&lt;210&gt; 166

&lt;211&gt; 713

&lt;212&gt; DNA

&lt;213&gt; Cercopithecus aethiops

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(713)

&lt;223&gt; n is a, g, c or t

&lt;400&gt; 166

cacgagaatt ctgtctcaaa aaaaaaaaaa aagccaaagg tcctctaaaa tggcctgcat 60  
 ggcactacat tctctggccc ttatcagca ctctgacagc tctctccttt gcttattttg 120  
 ctctcattc tagcctctgg atctttgccc ttgctgttcc ttacgctctt ctcccaggga 180  
 tctgaaaggc tcacaccctc acctccttca gaggtttgct aaaatgtctt ctaccagtg 240  
 aagccttccc caaccaccac attaaaaaca cacaaccagc acccgttctc tatcttcctt 300  
 cactttgcat ttgtccattg tgaacatca cttacatacc tttaattttt agtttattaa 360  
 ttcatactgc aaaacaactt agtttttacc atgtgccagg cattgtccct agttgctgac 420  
 aatacagttg aaaataaaat agacaaaaat cccatctttt gaatcttttg aaccttacat 480  
 tgggagtgac aggcaaaaac gaggtaaaat cagtaaaata cgtgagacag aacgtaaaaa 540  
 gaaaaaaaag aggaaagggc tgatttttgt gtcttccctt ccagaatgca agctcccttg 600  
 aggatacaga tttnngntgt ttttttacta ctgtatctcc tgacaanagg cgcccagtaa 660

cataggtang gcattcgatn ccaatttttn aaaatgagan actaggcagt tac

713

<210> 167  
 <211> 714  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(714)  
 <223> n is a, g, c or t

<400> 167  
 ctttcacgag aattctgtct caaaaaaaaa aaaaaagcca aagtcctcaa aatggcctgc 60  
 atggcactac attctctggc cttttatcag cactctgaca gctctctcct ttgcttattt 120  
 tgctcctcat tctagcctct ggatctttgc ccttgctgtt ccttacgctc ttctcccagg 180  
 gatctgaaag gctcacaccc tcaectcctt cagaggtttg ctaaaatgtc ttctaccag 240  
 tgaagccttc cccaaccacc acattaaaaa cacacaacca gcaccggtc tctatcttcc 300  
 ttcactttgc atttgtccat tgtgtaacat cacttacata cctttaattt ttagtttatt 360  
 aattcatact gcaaaacaac ttagttttta ccatgtgcca ggcattgtcc ctagttgctg 420  
 acaatacagt tgaaaataaa atagacaaaa atcccatctt ttgaatcttt tgaaccttac 480  
 attgggagtg acaggcaaaa acgaggtaaa tcagtaaaat acgtgagaca gaacgctaaa 540  
 agaaaaaaaa gaggaagggt ctgatttttg tgtcttcctt ccaaaatgca agctccttga 600  
 ggatacagat ttngtgtgtt ttttanttac tgtatctcct gacaatagcg cccagntcc 660  
 atagtaaggc attcgatcca atttttaaaa atggagatac tagggcagtt tact 714

<210> 168  
 <211> 792  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(792)  
 <223> n is a, g, c or t

<400> 168  
 ctttcacgag attctgtctc aaaaaaaaaa aaaaagccaa agtcctcaaa atggcctgca 60  
 tggcactaca ttctctggcc ctttatcagc actctgacag ctctctcctt tgcttatttt 120  
 gctcctcatt ctagecctctg gatctttgcc cttgctgttc cttacgctct tctcccaggg 180  
 atctgaaagg ctcacacctt cacctccttc agaggtttgc taaaatgtct tctaccaggt 240

```

gaagccttcc ccaaccaacca cattaaaaac acacaaccag caaccgttct ctatcttctt 300
tcactttgca tttgtccatt gtgtaacatc acttacatac ctttaatttt tagtttatta 360
attcatactg -caaaacaact tagttttttac catgtgccag gcattgtccc tagttgctga 420
caatacagtt gaaaataaaa tagacaaaaa tcccatcttt tgaatctttt gaaccttaca 480
ttggggagtga caggcaaaaa cgaggtaaata cagtaaaata cgtgagacag aacgctaaaa 540
gaaaaaaaaag aggaaagggc tgattttttgt gtcttccctc cagaatgcaa gctccttgag 600
gatacagatt tgtgtgtttt ttactactgt atctcctgac aatagcgccc agtacatagt 660
aggcattcga tccaattttt aaaatgtgat actaggcagt tactcagttt ctgggcacat 720
ttnaactttt agacnataat accgattaaa aaanccggtt ncagctaggc tacgatncaa 780
gananaactg tn 792

```

```

<210> 169
<211> 691
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(691)
<223> n is a, g, c or t

```

```

<400> 169
ctacgaacaa ccatgggtgag tagaaccatc tggattttcc atcactttca tttaaaagac 60
tctgttgata ttctaggtac tgattccata tatcagtatc aacaaatttc tcaaccaagg 120
ggataattgg tttatctggt tgcaattcat tccgtaattt agaaaggaga gaaatagctt 180
tcttttcagc ttccacgcct tccgtcaaaa atacaagaaa aatcaattgt gtgtgtgtct 240
gtgtctgtgt ttgtgtgtgc gtgtctatgc aattcctcta gggtaacata tttttacaga 300
cttaagaaga aaagaaaaat gttcaaaacta cattatactt ctttaaacat tacatttaga 360
actcttaaac tgaaaatcaa aaaacacaca cagatctcat atgaacataa tcatgcctta 420
tctatctaag ttctggcctt tctgtgtctt cggatgatcat tactacagag ggaaaggaac 480
ccctgacaga ttttccatgt ctttcatgct tccatacaca ttcttctttc accattgaca 540
ccactagaaa agaaactgtg gcctttctga ggtttctttt ggtagctcaa ttttttttn 600
aacttgtttt ccactgagtt ctagctaggt gagagatgag atatgctgac atacaaggcg 660
ctncaatatt atctnacatg acaggccaat t 691

```

```

<210> 170
<211> 699
<212> DNA

```

<213> Cercopithecus aethiops

<220>

<221> misc\_feature

<222> (1)..(699)

<400> 170

```

ctcaaaaaaa aaaaaaaagc caaagtcctc aaaacggcct gcatggcact acattctctg      60
gccctttatc agcactctga cagctctctc ctttgcttat tttgctctc attctagcct      120
ctggatcttt gcccttgctg ttccttacgc tcttctccca gggatctgaa aggctcacac      180
cctcacctcc ttcagagggt tgctaaaatg tcttctaccc agtgaagcct tccccaacca      240
ccacattaaa aacacacaac cagcacccgt tctctatctt ccttcacttt gcatttgctc      300
attgtgtaac atcaattaca tacctttaat ttttagttta ttaattcata ctgcaaaaca      360
acttagtttt taccatgtgc caggcattgt ccctagttgc tgacaatata gttgaaaata      420
aaatagacaa aaatcccatc ttttgaatct tttgaacctt acattgggag tgacaggcaa      480
aaacgaggta aatcagtaaa atacgtgaga cagaacgcta aaagaaaaaa aagaggaaag      540
ggctgatctt tngtgtcttc cctccagaat gcaagctcct ttgaggatac agatttgngt      600
gtttattact actgaatctc cnggacaaat agcgcccagc acatnagtan gccattcnat      660
ccaatttttn aaaatgagat actagggcag tnaactocaa      699

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<210> 171

<211> 767

<212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc\_feature

<222> (1)..(767)

<223> n is a, g, c or t

<400> 171

```

catctcacag agttacatct tcccttcaa gtaatccttt cgctaaggct gttcttgctg      60
aattggcaaa gcgatatttg gaagcccgta gagggtatg gtgaaaaagg aaatatcttc      120
cgttcaaaac tggaaagaag ctttccgaga aactgctctg tgttctgtga attcctcttt      180
tagaattttc ttcagaactt gtggcacatc attaaacctc cgtcagtgat cacatatctt      240
catcctttgg agtcaattta tttttggaaa cagtcaaaag tcaactcggag tgacttcagt      300
agaatgaagt gtgtgatcaa attggataaa aacttttttt ttaaatcaaa aatgagtaac      360
taaaaaaac agaagactaa attttctttt tgaggcatgt aaactggctc tgaaagaagt      420
tccaaataat tcaaagatgg ttttagcaat ggcagcactg ctgaaatcca tcagtctctc      480

```

```

aagggtgactt aaaaggataa atatcattcg gatgcataga gccaatccgg tccaccacct      540
gttttgtctg actcacatgc taagagtggg ttttatattt ttgaatggct gaaaacaaaa      600
gtgaaagaaa agtagtattt tgtgatacat gaaattcaaa tttcagtgtt cattaaataa      660
agntttcttt agaacacagc catgctcatt cttacatatt atttaaggct gcttttcaca      720
ctacaacgac aggnbcbagc agctgcaana aaaaccacat ggccccca      767

```

```

<210> 172
<211> 769
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(769)
<223> n is a, g, c or t

```

```

<400> 172
ctttcactgag attctgtctc aaaaaaaaaa aaaaagccaa agtccctcaa atggcctgca      60
tggcactaca ttctctggcc ctttatcagc actctgacag ctctctcctt tgcttatttt      120
gctcctcatt ctagcctctg gatctttgcc cttgctgttc cttacgctct tctcccaggg      180
atctgaaagg ctcacacct caccctcttc agaggtttgc taaaatgtct tctaccaggt      240
gaagccttcc ccaaccacca cattaaaaac acacaaccag caccggttct ctatcttctt      300
tcactttgca tttgtccatt gtgtaacatc acttacatac ctttaatttt tagtttatta      360
attcatactg caaaacaact tagttttttac catgtgccag gcattgtccc tagttgctga      420
caatacagtt gaaaataaaa tagacaaaaa tcccatcttt tgaatctttt gaaccttaca      480
ttgggagtga caggcaaaaa cgaggtaaata cagtaaaata cgtgagacag aacgctaaaa      540
gaaaaaaaag aggaaagggc tgatttttgt gtcttccttc cagaatgcaa gctccttgag      600
gatacagatt tgtgtgtttt ttactactgt atctcctgac aatagcgccc agtacatagt      660
aggcattcga tccnattttt taaatgagat actaggcagt tactcagttt nctggggcca      720
tttcaacttt tagacaataa taccgatnag aaaaacggtt acagctagg      767

```

```

<210> 173
<211> 769
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(769)
<223> n is a, g, c or t

```

```

<400> 173

```

cagagaacac agnagtcagt ttctcagaaa gcttctttcc agttttgaac ggcaagatat 60  
 ttcctttttc accatagecc tctatgggct tccaaatata gctttgccaa ttecacaaga 120  
 acagccttag cgaaaggctt ctgaaggga aatatgtaac tctgtgagat gaattctacg 180  
 atacatgtaa cattctacga acaaccatgg tgagtagaac catctggatt ttecatcact 240  
 ttcatltaaa agactctgtt gatattctag gtactgattc catatatcag tatcaacaaa 300  
 tttctcaacc aaggggataa ttggtttata tgtttgcaat tcatccgta atttagaaaag 360  
 gagagaaata gctttctttt cagcttcac gcttctctgc aaaaatacaa gaaaaatcaa 420  
 ttgtgtgtgt gtctgtgtct gtgtttgtgt gtgcgtgtct atgcaattcc tctagggtaa 480  
 catatlttta cagacttaag aagaaaagaa aaatgttcaa actacattat acttctttaa 540  
 acattacatt tagaactctt aaactgaaaa tcaaaaaaca cacacagatc tcatatgaac 600  
 ataatcatgc cttatctata taagttctgg cctttctgtg tcttcggtga tcattactac 660  
 agagggaaaag gaacctctga cagattttcc atgtctttca tgcttcata cacattcttt 720  
 tttcaccatt gacaccactn gaaaagaaac tgtggccttt ctgagggtt 769

<210> 174  
 <211> 784  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(784)  
 <223> n is a, g, c or t

<400> 174

cttcaaatgt tgaaaaagag ctgaaatgct gcacagctga atgaaggatc ttctcaaggc 120  
 tctcctggcg cgagccaatc ccagcctcat gaacgagaga gatcctgaca cccacagatg 180  
 ggcacctcac agccacatgg agacagagac aggcctcgtg accagccacc ctacagacca 240  
 cacggggaca ggctcgtgta ccagccaccc tcacagtcac acggggacag cctcgttgac 300  
 cagccaccct cacagccaca tgggacaggc tcggtgacca gccacctca cagccacagc 360  
 gggacaggct cggtgaccag ccacctcac agccacacgg ggacaggctc ggtgaccagc 420  
 cacctcaca gtcacacggg gacagcctcg gtgaccagcc acctcagag ccacacgggg 480  
 acaggctcgg tgaccaggca cctcacagc cacacgggga caggcttggt gaccagccac 540  
 cctcacagcc acacggggaa cagctctcgg tgaccagcca cctnagagt aacatgggga 600  
 caggctcggc tanccagcca cccctcacag ncacacgggg gacngggctc ggtgaccagc 660  
 cnacnctnac agncacaocg gggacagggc tnngtttacc agcccacccc tcacagaccn 720



cacgggggac aggggtttcgt ngaccagccc acccettaca ntccacacgg nggnacagcc 780

ctcg

784

<210> 175  
 <211> 733  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(733)  
 <223> n is a, g, c or t

<400> 175  
 aatgtgggaa atgcatcatt tgaaacattt taatggagag actagtattt gatataattaa 60  
 tgttaggttc ctccagaac ttaattttta aaatttttat ccaaacttat ttactttaat 120  
 tatcaccatt tattgaatac attaattgaa atagctcagc tcttctgacc tgtggagcaa 180  
 aggnntgacc ctgaggatct cctggaagct gccctcaact aagcagaact cagaggaaac 240  
 ttttgactga gaaactgagg tgggtcaaatt gtgctaattgt taaaatacat aaaatagaac 300  
 atttctttca atcagaacta ctgacactat tacatggcac aggttgccag ttactctgat 360  
 tagaaatact aaacagaaaa aagaaaacac ttggcttgga tccttaaaga ggtatttacg 420  
 gaagggtgtg ccaacacagc ccacccaat gtctggtgag atttctgtc tgggagaggt 480  
 ctatgggatc tcacccaaac accacagacc ccagtagcat ttctggact aatgttcttg 540  
 tcttttcaca gtgctctgct gatttgggtct ttagataacn tgggtcttct tcctcttcat 600  
 aggnatctat acccctgaa gtgtgggtcc ttagactcag ggggcttctt caaaagccct 660  
 tttggattca gnanaaaaag aancctgggc acttaactgg ggctnaaaga aacacttctn 720  
 ccgggttccn caa 733

<210> 176  
 <211> 729  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(729)  
 <223> n is a, g, c or t

<400> 176  
 catgtccttt tcagtaacat ggatgtaatt ggaagccatt attctaagcg acattaatgc 60  
 aggaaaagaa aatccaatac cacatgttct ctctgtaaa tcggagctaa acattgggta 120

```

cccagggaca caaagatggg aacaatagac attggggatt ccaaaatatg ggatgtaggg      180
aggagggaaa ggatttataa agtgtctatt gggfctacg tttagtacct ggggtgbcgag      240
atcatttgta ccctaaacgt cagcattatg caacatacca atgtaacaaa cctgcacatg      300
tagactctga atctgaaagt tgaaatactt tttaaaagtc tattatatta tcacacaatg      360
accccataaa caacaacaaa aaaaagtgaag agtaaaaaaa cgcaagggtct ttagacgtag      420
gaatcagaat gatataaaga aggaaaagag atttatacta atatagaacc ttttttagaca      480
tgaattttta aaaaatgata cctagggttat caagttactt ttgtgtccac ctaaatattta      540
tacctgtat ccctaaccac aattggctgt attttgaaga cagagccctc aaaggaagta      600
attcagggtt tggtgtccct ataaggagga gaacactagn agnatctcag cttctctcca      660
ccccaccccc aaccccccaca aaaacatggt aaagaaagnc tttatnttgn gggacacagt      720
nggagaaaaa                                     729

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<210> 177
<211> 679
<212> DNA
<213> Cercopithecus aethiops

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```

<220>
<221> misc_feature
<222> (1)..(679)
<223> n is a, g, c or t

```

```

<400> 177
catgcaaggc caggtgcagg catctcttcc aatagggcag tgtctaccag gtagggctct      60
tctctcttta gaatcattna tggaaatata attcacacaa cataaaattc acccttttaa      120
actatactac acacacacac acacacacac acacacgaat aaaccatata ccattagcag      180
ttattcaaca cactctgccc ctttgacccc tggaaataat cactaatcta ctggctggta      240
ttatggattt gcttattctg gacaaatcat agaaattgaa tcattaaaca tttgggttatt      300
ttgaatctat cttctttcac ttggcataat gtttgcaagg tttatccatg ttgcagcaag      360
taccaatact cattcctttt tatgcttcca taatattoca tggatatatt ataatttttag      420
tcaattttta agtcgggtgaa catttacact gtttctcctt tttagctatt atgaataatc      480
ttgctatgaa tattcatgta caagtttttg cataaacacg tttncaatc tctattatgc      540
acctagaagt ggaattggta ggtcatatgg taattctatg ntnaactttt gngaatatat      600
gccaaactat ttcccaaagc aactgcaccc atttngtatt accaccatta aggnataaaa      660
ngttcctact ttcttcaca                                     679

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```

<210> 178

```

<211> 737  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(737)  
 <223> n is a, g, c or t

<400> 178  
 ctttcataat gaaaagaaaa aaatgaattt caactagtat cgatttttcg gtgtgtgggg 60  
 gcagggcatt taagggtatt atttcctagt aatgatcact tagattctaa gccttaaaca 120  
 tgattcaaat gcagcagaaa tcaggaaaga agcaacagat acgggtgtgc atatcgaatg 180  
 tctagactac aaggcaaaac ccaaatacca agaagcatc catgtgtcaa accagcataa 240  
 tttctaagct atgcctgggg ccacatacaa aaaaaaaaaa aaaaagggtta gtttgaaaga 300  
 aaaatctagg aggggtaacc agaagggtcaa cccagttca caggaactgg gaagaagcta 360  
 gccgttacct tgtgacatct tctgagcag ctctctcgc agccagctcc ccagcctcct 420  
 tacaatgttt ccaaaaggcc caactcccta aacatttgct tcttcaaggt catcctaaga 480  
 taaggcagtg aataaccacc aaacactgag tcacggatac ctttcggcta aaaaagatcc 540  
 cccttcccaa aatcattaca taaatacttt aaatgccaaag aggggtttct ccggaactcc 600  
 accagaaact ccagnactt taatttagat tgggcaacta aatgtgttca anttttgcgc 660  
 cataaaatat taaaggcttt tcagggtctgg caantncagt tcaaaacagg tgctttcagt 720  
 gtacgctgaa taacagg 737

<210> 179  
 <211> 759  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(759)  
 <223> n is a, g, c or t

<400> 179  
 cagatttttc ttaagaatt ttgtttattg caataggatt atcaaagtaa aaattaaaaa 60  
 gtaatgaaaa aaattaaaaa ataattttgt agctaccctt cctataaaac ttatccagat 120  
 tacttcttga octatacttt gagagcagag gaaatctagc tacattaact cagtagctct 180  
 gcaacttcta ggtaatttct tacctgaaca gtatatccta agtactgtaa ttcctgcatt 240  
 gcttgacat ttgagtttat tattocatcc ctgtattaca ataaatattc ttacataaa 300  
 ctttcaagag aaaaagcatt caaggatatat gtgtgtgtac acacttatat atatgtgtat 360

```

atatactcct gtaaaccata attggagttt aaaaaatata tggatattgc aattttctct 420
tctttctctc tgtctctctc tctctctctc tctctctctc tctctctctc tttcgatgga 480
gtcttgcctc gtcacccagg ttggagtgcg gtggtgtgat ttcagcttac tgcaacctcc 540
aactcctggg ttcaagtgat tctcctgect cagactccca agtagctagg actacagggtg 600
cgtgccacca tgcccggcta atttttttgt attttttagta gagatgggggt ttcaccatgc 660
tgnccagact gntcttgaac tccctgacct tctgatccac ccgectcgtc ctcnaagtg 720
ctgggataca ggncatgagc caccaccccc gccggattt 759

```

```

<210> 180
<211> 770
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(770)
<223> n is a, g, c or t

```

```

<400> 180
cagcttttat atatgctgag ttcaagacac ataagtacat atagataant aatgtacact 60
tcttctgtaa gaagacatat aagactgtaa tccatgagag aggggaagtct aagatgacat 120
gtttgggaat ccttttatatg gacatgatag atgaagocaa agagaacaat gaaatgattc 180
atgttgagtt atttgacatt ttaaaaagta tataagtatt ttaatagtgt gaccatttgt 240
gtctggaaat ttgaaaagc acaaagatct acaatgattt atttatctct ataactgatct 300
gtaggaagtt tttggcatgg gaaattgtgc taatgagtat ttggaaacaa gtgtattaaag 360
taagggttta caagatcatt agactttcat tttgcagact caatcagatc tggtcactat 420
agtctcctgt tggcataatt ggtttcctga ggacttatta cctgtagatg cacaattttt 480
cattccaaca atgttctgca ttccttttgg actttcctgt cttgaggatc tctttaaaga 540
gctaaaacct caggaacttc ttctacttgt ttctttaaag tcaggatgag agacagaata 600
agggatccag ccatgatggg tttcccccag gttcttctct catgctaagc cctttatggg 660
acgatgtgcc tctcaaagga gaatgcagat ctaatactat tgcaccactc tgaaagaagt 720
atgaggagaa ggcanaagag ctatgaaaag aaaaacatcc tgatcttttt 770

```

```

<210> 181
<211> 706
<212> DNA
<213> Cercopithecus aethiops

```

<220>  
 <221> misc\_feature  
 <222> (1)..(706)  
 <223> n is a, g, c or t

<400> 181  
 ctttcatgcc tagtaaagag tggggccttgg cctggagagg gaggcctcat gggccagata 60  
 agggagatgc tggcccatct gggcacgcat gtgcccgtag gctttccctg tcgagatgat 120  
 caactggaaa ggcagagaat gcggcctgga ggctcagaaa catccttgaa gccatatccc 180  
 caggtcctag tcctaactgc cactcttttc tttttttgaa atggggctct gctatgttgc 240  
 tcaggctgga ctccaactcc tgggcttaag cgttcctcct gcctcaactg cccaagcagc 300  
 .cacaaaccac acctggcctc ttctgccac ttctagctta gcagggtggt tcatctgtat 360  
 acggggatga cgtgactgct tgggggaatg agctgagccc ttggtggaat catggttcat 420  
 .gcaagaggtc tccggcaaaa tgctccaggc ttggagtctg ctgggcgctt ctaccctga 480  
 caatccgttt acttaaccacc acctctgtt cagacaggga agttctttcc atcaggatta 540  
 tagcgaggat tggcttctcat ggcacccttg gcacccgagc acgtgttggt ggagctgttc 600  
 tacgagccag gacacaccag ggaacggttn cccgcaataa acaccgtct cttcctcgta 660  
 ctcaagttct tcgggggttg aacattctga gagcttgctc ttcatt 706

<210> 182  
 <211> 740  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(740)  
 <223> n is a, g, c or t

<400> 182  
 cngngnctcg atcgttcctc ccacctcagc ctcccaaagt gctgtgttac aggtgggagc 60  
 cactagaccc agctgaatta tggattttta aggctgcttt atgtcaaaca ttgcgggttc 120  
 ttttaatatatt gttttccaga tttaagattt ttttctttta agctttgtat aatttatagt 180  
 aatttggtaa agtacttttg aaaacaaaaa tgaaaacatt tgcttttctt ctctacctga 240  
 acctccaga atttagaagc aatttatgat tattcttatt ttacagcaa catgggtatt 300  
 tgcatagggt cagtaagaat ctgttctctg tccaggcaca gtgggtcaca cctataatcc 360  
 .cagaactttg ggaggctgag gcaggcagat cacttgagat caggagttca agactagcct 420  
 ggccaacatg gcgaaacct gtctctaccg aaaatacaaa aattagcctg gcgtgttggg 480  
 catgtgcctg gaatcccagc tactagggag gctgagtcag gagaatcact tgaacctgcg 540

```

agggtggaggt tgctgtaagc tgagattgta ccaactgcact ccagcotggg tgacagagtg      600
agattttgtc tcaaaaaaaaa aaggagggcc aggcatagtg gtcctgcct gtaattccag      660
cactttggga gaccangggg agcgaatcac anggtcagtt cgaggtgact ntaggganaa      720
aattatgttt naatagaaaa                                740

```

```

<210> 183
<211> 720
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(720)
<223> n is a, g, c or t

```

```

<400> 183
aaacagtaaa aaataaggaa ttttactttc tctggggctc ccaggctctc tggttggggtc      60
agggcccaag tggagcaggg aagaaggggc cactctttct gaagtctccc tgcataaatg      120
aaaataacag ttgagtggca gtcacacact tagaagcaaa tcattctgat ttgtccttct      180
agagcagaga tgtctccct aagatccatt ttaccccagc agaaaaagcc cgggttggtct      240
ggattgtagc aacgctgttt tgacagaaag ccctatgatt tttctcacia acttccttaa      300
ggatgctatc tttcagctac acatacttag attatttctt ctccctcacc aactcaatct      360
aatgttgcta aggggttcag tactttctct ctgctgctta cctcgtoeca acccccaagt      420
tctttcccaa attccagcag ctgggaccag tctctgggac agagcagaaa taacatggaa      480
attgggggta ggggttaaaca catctatcag tctaggaaca ggtagaaaag caacaccccc      540
gtgactacaa gtttggtagt gggcaacaat tttcttatcc atcatgggtg gtgggtgtggg      600
tagtnattga gcataanttt atttgtagag gtgaatttgt ttactgggct ntnaagggct      660
acatggaggc tgtccaagga aaganattcn ataatnaatg gaaatttatt ataatttaat      720

```

```

<210> 184
<211> 775
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(775)
<223> n is a, g, c or t

```

```

annnnactna nnnnnnnnat tggctnnttn nnttgggggg naanccagta cttcaaaact      60
ttgtattatt taataaatga tactgactag ttggctaaac attgaacaa aagataaatc      120

```

```

tctaaaccat tctaccacc aaaataaatt ctagaaatga acaaagattt caaagtaaga 180
agtaatccac aaaagtacgg aagaaaacaa tcttaaattg gagaaggact ttctaaacat 240
ggcaccaaag gtagaaacca aaaggaatca ctgacaggtt tcatcacata aagattttta 300
aatttctata catccaaagc actacaatgt tcagctcaag atggcaggct aggcacattt 360
gcctttcatc tttagagaac catttaaata aaaagacgga ggtacaatga ggaaaaactg 420
taacagggaag gagacgggct ggaacgacag gaagcagatg agccagctgg gagatgaacc 480
agctgaaaga gctgcagtgg agatgaaagc ctgtcctgtg canactgtgg aggaaggagt 540
gaaagacccc acctgtaggt ttggcaagct agctgaggat cgttncncat gattgaacaa 600
natggattgc acnctggtn tcnngcnnnt tgggtggana ggctntnnn nttntantgg 660
nccaacanac antnnntgt tnatnccnc cnnntncngn tnnnannan gggcnocnn 720
ttttnttnn ananccact nnnnnnncc cnatnaact nnnnnnang nnnnn 775

```

```

<210> 185
<211> 400
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(400)
<223> n is a, g, c or t

```

```

<400> 185
tttttcccg ngggngnnnn nnnnnnnnnn nnnnnnnncc ccccccttn nnnntgggg 60
gggggggaan nneccccccc ctttnnnnnn ttttnnnng nnnngnnac aggttttttg 120
ncngggggat nntnttanc ccannntttt nnnnagngng gnnnnnann nnnccagcnn 180
ggngnnannn tgctnnctg cncgnnncca gcccgctct tnnctgnta cagnnnnntc 240
ctnattgnac ctccgctnt ntatntaaat ggntctctaa agangaaagg caaatntttt 300
tttctgcca ttttgagcng aacattgng ngctnnggat gnatagaaat tntaaaanct 360
tnntgtgang aaaccngcaa gtgntttttt tnnngnncc 400

```

```

<210> 186
<211> 951
<212> DNA
<213> Cercopithecus aethiops

```

```

<220>
<221> misc_feature
<222> (1)..(951)
<223> n is a, g, c or t

```

<400> 186  
 ccgccnggtg ntgggaaaga cnnnggacgc ttcagaccac aggnaggtag catcctggaa 60  
 cctggaatct ggaacctcag gggctgacct ggcactgggt gggcctggaa cctgtatctg 120  
 cagcccagaa gcaggggtctg caggtgcaag cctgatgoca ggctgcaggg gacagccng 180  
 agcnggtttt tnttgaggca gggngtgata angccagcag gcccaaagca aagntaggg 240  
 cnnatntntg ttcctaacc ccatgcngag gatacctnnn ttnaagctgc ggagocngag 300  
 gaagggaggg ggccgacga agagaatgtc anaactance ttncnnacct nctncagngc 360  
 nacctccagg ngctgtaanc actcactagg anacccttaa ggnccnactg aaaggagcnc 420  
 ccctangagn gatggnagca aaaaananga nacgacactn cgactgcngg gngacgtgca 480  
 acntggaaag actctgnncc ctncancacc tcgggnanac tatnacaag angncccca 540  
 ncacctncan aatgaaagna aangtgancg ngcnanacca acnncgacnn ccctnggcca 600  
 agagaacacc aataacnaga ntagganatc caaaagcggg aaanacnaca gngctatnng 660  
 gaatgcncaa gccaccatnn cttgcantgg nncacagnt gnaatcnaaa nctacnnccn 720  
 cnatacactg gagagacaan naccnagcnc cantaaagcg nnaaaaanga gaaaacgnaa 780  
 aaaaancgcg anngnngcng ncnaatngcc cnnacntaa ccctccnnan aaaaannaat 840  
 cngaacctg gnnacgacnn ncnaagnggc ncaanccncc cncaggcgnc tcnccncc 900  
 gccacnanca cccngagcc ncncagagn caccngcctn acncacccan c 951

<211> 450  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(450)  
 <223> n is a, g, c or t

<400> 187  
 tncntnttn ggggtnnan nnnnnnnnnn anntccncca atnnnnntgg gggggaannc 60  
 ctggttctct gactctccc tcttttcac tcatgtcgcc aggttccca aatgttccct 120  
 gactattctt tccctttttt gtgcccacct gtgcccagg cacagcatgt gacctagtc 180  
 tgggagtcgg cgggtggcaga actgcaggcc gttggggcct ccaagtagac catgcaagtt 240  
 tcacagccat attnctctga taccagaagc taaggagtgc tgcctggcca gtactaggat 300  
 gggggtcgcn ctgggaacac tgggtgatgt aggttttttg ctacagcnc cctccctctn 360  
 tccccctnca gnnngcctnga tncacaacca tncctgact ntntntnctn ntntnnncc 420  
 gcaactgcat ncnanacaca nncngngact 450



<210> 188  
 <211> 338  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(338)  
 <223> n is a, g, c or t

<400> 188  
 tncncttnt gngggannna nncnnnnnnn nnnntccnc ctnnntggg gggggaannc 60  
 gnnacntnc nntttangaa agagacgacg ctncgagga agaaggttn tgggacgagg 120  
 gactgggnag agctccagag cccagcagc cgggtcaag gnccttgcg cataggcgcc 180  
 ccaccngac gncagggacg cgactnccgn gangccccgc gcgcggnng anccaggcg 240  
 cgggcnnaga ctngatcnn ggagngccc ngngccnnnc ngacggngcg nnnngnggn 300  
 cnngggcgcg ggcnnngnga nnggacagnc nggagcnt 338

<210> 189  
 <211> 936  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(936)  
 <223> n is a, g, c or t

<400> 189  
 ttttnngggg gaannnnnnn ngngtangn rnnnnnnccn ccgcggttnn nccttggggg 60  
 gggaannncc nnnccangtn ncttttcat gnaaagnna cgacgntctc cgaggaagaa 120  
 ggctccggga cgcgggactg ggtagagctc cagagccca gcagcccggc tcaaggcccc 180  
 ctgcgcatag gcgccccacc gtgacgtcag ggacgcgact ccgcgatgc cccgcgcgcc 240  
 gtctgatecc aggcgcgggc tcannntttt atctcgaggt tccccctgcgc ctctctgacg 300  
 gtgcgttctg gcggcctcgg gcgcgggctc tgcgatcgga cagcctggag cctttggcct 360  
 cgatttacat gggaggccoc tcgaaacagg gcacgtcact tgccccggg cacctgcgga 420  
 cggggagact ctcggttga ctccaaggcc tgacattccc ctccggtttt caccgaggag 480  
 gatgaggatg ttgtcaggag ctgcggcaag gctggaggag ctgctgtgn gtccaccnc 540  
 ctctgnacag gccttagcat ncaccncag tttctccctt gacttntgaa ccnaactcc 600  
 ttacccccgc aagtnncnn cctgtttnga ttgtgaaac tgcaagtgc ggaagantaa 660  
 aatgtttgcc naagctnat gcttnanggn gntgcccngg gtataaggtc anggggtggg 720

ggcccttnc cctgnnggt nggcnttaag ntaaccagg gnncttggca ntnantnt 780  
 attcaanana tgccanggn ntcggnntnn aangntntt tnnanaaaat nnttncctt 840  
 nttannctnt annccnagg gaaanccntn gggcttgtt tngccctgna aanacnatna 900  
 aaggggtaat nccccncct tnaatntnnn gncncc 936

<210> 190  
 <211> 936  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(936)  
 <223> n is a, g, c or t

<400> 190  
 tttttngng ganncnnnn gttntngnn ncccccccc ccatnnntt ngggggggaa 60  
 nccccnnca cgtcctcntn atgaaagaga cgacgcctcc gagaagaagg ctctgggtac 120  
 gcgggactgg gtagagctcc agagccccag cagcccggt caaggtcccc tgccgatagg 180  
 cgccccacgc tgacgtcagg gacgcgactc ccgcgatgcc ccgcgcgcgc tctgatccca 240  
 ggcgcgggct cagantnna tctcgaggt cccctgcgcc ttcctgacgg tgcgttctgg 300  
 cggcctcggg cgcgggctct gcgatcggac agcctggagc ctttggcctc gatttacatg 360  
 ggaggccct cgaaacaggg cacgtcactt gccccgggc aectgcggac ggggagactc 420  
 tcgggttgac tccaaggcct gacattcccc tccggttttc accgaggagg atgaggatgt 480  
 tgtcagygac tgcggcaagg ctggaggagc ttgcgttggg tccacccgcc tctggacagg 540  
 ccttagcatt caccgcagt ttctccctga ctttgaacct aaacteccta cccccgcaag 600  
 tccttccctg ttttgattgc tgaactgcaa gtgacggaag aattaagtgt tggccgaaag 660  
 ctgatgcttc agggggtgca ggntagaggt caggggtggg ggccctngct tnggngngc 720  
 atantgtanc ccanggtccn gactgantn ttnnaggaat gcanggaatn gnatannang 780  
 gtntaanaa antntcccc tannaactga taccnnagna accntngggc tgnntgancn 840  
 tgaaaaaccc annagggtaa ngcctnnctt atnngggccc cnnntnctnag annaaangcc 900  
 ctgggggttc anngaaaacc cnnnnanaaa ntntgg 936

<210> 191  
 <211> 951  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(951)  
 <223> n is a, g, c or t

<400> 191  
 ttttttngng gancnnncng gttgttggnnc cntcccgccg attcccttgg gggggnaacc 60  
 cccnnncang tncctnttna tgaaagagac gacgntccg agaagaaggc tctgggacgc 120  
 gggactgggt agagctccag agccccagca gcccggtca aggtccctg cgcataggcg 180  
 ccccaaccgtg acgtcaggga cgcgactccc gngatgcccc gcgcgccgtc tgatccagc 240  
 cgcggggtca nanttnnate tcggagtcc cctgcgcctt cctgacggtg cgttctggcg 300  
 gcctcgggcy cgggctctgc gatcggacag cctggagcct ttggcctcga tttacatggg 360  
 aggccctcg aaacagggca cgtcacttgc ccccggtcac ctgcgacgg ggagactctc 420  
 gggttgactc caaggcctga cattccctc cggttttcac cgaggaggat gaggatgttg 480  
 tcaggagctg cggcaaggct ggaggagctt gcgttgggtc caccgcctc tggacaggcc 540  
 ttagcattca cccgcagttt ctccctgact ttgaaccaa actccctacc cccgcaagtc 600  
 ctccctgtt tgattgctga actgcaagtg acggaagaat taagtgttg cgaaagctga 660  
 tgcttcaggg ggntgcaggg tagaggtcag ggggtggggc ctgccttgt ggngtcata 720  
 tgtagocag ggtcntggca ctgattntta ttagaatgc agggantng attagatggt 780  
 ttcttagaaa atatccctn tgnantgnt acctgagnaa ccgctgggct ggcatnacct 840  
 tgnaaaacc agaanggtta nngcccttc ttantngtg cccnattttt tcaggacnaa 900  
 angggccntg gntttncat gnaatcnct ttgcncaaan nctggttc t 951

<210> 192  
 <211> 938  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(938)  
 <223> n is a, g, c or t

<400> 192  
 ttcnngntc ttnntgntan attttcccc cattttttg ggggggaanc cnacnca 60  
 aaaggtagaa attattgata aantntaaat gttacaaact gcngctaaaa gaagcaaaag 120  
 agaacatgct gtatgatect tttttttttt tttttttttt tttttttgag gcggagtttc 180  
 actcttgttg ccaggctgg agtacaatgg cacaatctcg gctcaccaca acctctgect 240  
 cnnnttttca agcaattttt nttncttann ctccctagta gctgggatta taggcatgtg 300

ccaccaggcc cagctaattt tgtattttta gtagagacgg ggtttctoca tgttggtcag 360  
 gctgggtcttg aactcccgac ctcagggtgat ccaaccgcct cggtctccca aagtgtggg 420  
 attacagacg tgagccactg tgcccggcaa tcttttttct taattttaaa ttttttagag 480  
 acaaagtctg gcttttctag tncaggctg gagggcagtg gagccatctt ggctcactgc 540  
 ancccttunc tcccaggctc aagccatctt nctaccttaa ncttctgag tngctggnaa 600  
 ctacagggtac acaccaccat gtcagnctaa tttttttttt tttttttttt ttgaaaccna 660  
 attttttcnt tgttccccc tnnatgganan ncaggngnaa nnanctctnn ccnctcnac 720  
 cccttacnnc naagnncaat atnaantatc nncctacnnn cccnagntct tnnntttta 780  
 annnannttn tatttttntt nnttatantt tacctnnntn tttctnnntn ctnanccctn 840  
 ntncactnnt nnactantct ttttccactt attcttctct ncnctntnc tnatatcn 900  
 nncnnnctc tctctntnc tctttnttt ctnnnatn 938

<210> 193  
 <211> 804  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(804)  
 <223> n is a, g, c or t

<400> 193  
 tntnggggt nnnaaaacnt tncnnacata atcgccncaa tacaanttgg gnggggaaaa 60  
 annctgnntc attcctcctt gnacccatct ccatgccgtg naagcatctc ctncctggac 120  
 ttgcactatc tgggtccata gcccttgctt attcttaaatt gggagtcact ctgacttgca 180  
 ttgtggggaa ggtatacct ggggcacagt cctctgggat ggacacttcc ataggaaggg 240  
 gcagttatac gtggacttat gtctctctac actctcatcc agaaccatcc acccagaagc 300  
 aggagtgtgt tcttttagaa accagccggc ccaatcagcc cattttatag gtgaaggcag 360  
 tgaagcccag agagataaag catcttgctc aaggtcacag agccagacct agactaggct 420  
 gccctggctc tagttcaggg ctcacccac cctagccggc ttctggctag acagaatcta 480  
 cccatcttgg ccagactct ctgggtgggaa gtcagggatg cagnggtcag gatgggcatc 540  
 agagccagca ggcctgagc acgntcacc caagtggaa atgaacttcc taaactccag 600  
 nggaagttag aaatggcana ttgatcagng ctaatgagct taaaacaccc agggattaaa 660  
 aaaaaaaca tgaanaagct ntacttnaag cataaatntg ntnaacanaa agganaccng 720  
 gctnncnnt ntntnanann nacnnnttg aggctnaggg ggnngnnaa tnnngngn 780

gapattngnn ttngnaaggg gnnt

804

&lt;210&gt; 194

&lt;211&gt; 560

&lt;212&gt; DNA

&lt;213&gt; Cercopithecus aethiops

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(560)

&lt;223&gt; n is a, g, c or t

&lt;400&gt; 194

ttctanttnn nnnnggttnna ancannnnnn ncatnntcgn cncatnnnnn ttgggagggg 60  
 aannnaatna ataatcaaan ttagnaattg aatttagaat ttcatttatg aataaaaagg 120  
 ctgggaggaa acacacccca accgacacag tggatgcgat aggataagac tatgagcaga 180  
 ttttgttctt ccttttcacc gtctgtattt tccatcaatt atttgtatga ttaaaatcaa 240  
 tcatttcaga caagagggac attgtgagct atctgtgaga aatgtcttct atctgtttcc 300  
 agatagaagg ggctccagct cggtttgggg aaagtcccaa tgccattctc ttaaccaaga 360  
 ggtttcctac ctcatctaatt gtggagattc tacttaccgg ggaagactcc cctcctgtta 420  
 cctcaagtct gcagccggcc tccagactt ctgectnctn ctaaccacag cctgcctggn 480  
 tgcaggncgg ngggaaagga gggcatangg ggctgnatnc cgnaaggcc ctnncaactcc 540  
 tngactnang cagggnnctg 560

&lt;210&gt; 195

&lt;211&gt; 977

&lt;212&gt; DNA

&lt;213&gt; Cercopithecus aethiops

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(977)

&lt;223&gt; n is a, g, c or t

&lt;400&gt; 195

cnnccccng gntncccneg ggnnnnnnnn nnncccccc ccnanncttt ggggggggaan 60  
 nncnnncctt tnggnagnatt gnnnggnana annngtntct tcnnaatag natngggcng 120  
 canttcaact ncgctaatta acggaacagc aggtngnaa ttctgacaac agcaggacac 180  
 aaanggggcn gggatcagca ctgaatgccg gcgaagcatg ccccccccc ttaagaagaa 240  
 gcacaacacc cagacccac attnnntntn gggncaggtc catgaaggng cnaacctnga 300  
 tttagttana ngcnctnccc tgcagcaact ccaagggcnc agggttttta aaatgncnc 360  
 tcaggccttc tttagaggna gcaagccngc cccaactggc ctttttcenna aaaaagangg 420

aaacaggnc t gngattggc nagagcagga nncgcccagc ccnttnggt ccccnngggc 480  
 acacngnaag aaaaagaatn gnnttggacc acacagaaaa cacaccaana ctaangacag 540  
 ctgaaaagct caaaaaaaaa atcgcnaaaa aatccctcaa tgctcnaaga agtccncaaa 600  
 nncgcccngn gacngnnaca cagctnccng gcncgcanga cncnnggggn ncacaggnng 660  
 cnacacccag gaccagnagn taatatcnna aaagggtaac aanaaaancc ctaataccaa 720  
 aaangcnatg anaatggaag cnnnacncc tncaaaagac aagccctang gaaancntcn 780  
 cncnacccnn nccccaacn ggcanncggg ccccaccca aaaggggggn nccgccccgg 840  
 aannnaaaan ccnacnnngg ggaaaaanng accnnaancc ngaaanngtc tatancccca 900  
 cngnccnaaa acctccang ncaatnaacc cncctccta aaaggntagg annaanaacnc 960  
 ngnggcaaag ncnacca 977

<210> 196  
 <211> 868  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(868)  
 <223> n is a, g, c or t

<400> 196  
 gaannccnnc nnaaaaaacn nnnnncccc nccccatann ncttgggggg gaaannnccc 60  
 ccccaacagn natantnagn aggnaggaaa acacanttaa tatatctcac tagcnctcat 120  
 ttccctcccc caccctcatc ccactccact gctaagagag agaaatnca gcaactgctat 180  
 cctgttntat tatacatntt cccttngag tnaaggattn naagattnng aaagtaacag 240  
 aatagaaacc aaaagtnta ctcaactncc aatttggctt aaaaagagag aaataatnat 300  
 tattnccat gnnacccaaa actnattctg nnaataacag ntataattat atattcaaan 360  
 naataaatga agatcgcaa aatcacctna atataatnng nagcagctaa agaacaaaaa 420  
 tnnnnnncat nngctnctat aagnagacat cacatganna ctncatnga ccagnaagaa 480  
 actagnaaaa ncaggcagnc acctaccatn cnnnctaac annnnnnnc nnnnctatn 540  
 caaccnnnnc ggnatanncn naagaagcca aatcaagaaa nnagaccnnc atgcctaaaa 600  
 aaaaanngng nnatcnnaan acatcangaa caggaaccng nngnanataa cacaggnann 660  
 caaagcnna ncncaannn cnagaaccn naacanaaa ggcagcnnan anncaagann 720  
 agaaacngaa nncacanaac acanagcann nncnanaaa gcnnnnnca nnnnngaacy 780  
 aagaaannnc nnnnnacca aggcncnaag ggcnnncaaa nncnnngcc aannnaaaaa 840

aaaccnanca aaggcncnng anggaaaa

858

<210> 197  
 <211> 260  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(260)  
 <223> n is a, g, c or t

<400> 197  
 ttttcnggng gannnnnnnn nnnnnnnnn nccnccnccgn tnnnttgagg ggggaaannc 60  
 nnnncacang nnatnttngn ggaggaaaac acatttaata nanctcatta gccctcattt 120  
 ccctccccc ccctcatccc actccacngn taagagagag aaatnncagc actgntatcc 180  
 tgnnnnatna tacatttncc ctnnngagtn aaggatnna agatnnngaa agnaacagaa 240  
 nagaaccaa atnttttttt 260

<210> 198  
 <211> 901  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(901)  
 <223> n is a, g, c or t

<400> 198  
 ggganancnn agnngnaana nnccaacccc gccaanatnt anggggggan actntcacia 60  
 gtatacaaga ggaggaaaac acaattaata tatctcacta gcattcattt ccctccccc 120  
 ccctcatccc actccactgc taagagagag aaatttnggc actgctatcc tgtntatna 180  
 tacatnttcc cttttgagtn aaggatnna agatnttgaa agtaacagaa tagaaaccaa 240  
 aagtttntct aactnccaan nnggctaaaa agagagaaat aatnattatt toctatgna 300  
 cccaaaactn annngnnaa taacagntat aattatatat ncaaataat aaatgaagan 360  
 cgccaaaatc accttaatat aattgncagc agctaaagaa caaaaanncn nncannngc 420  
 nncnataagn anacatcaca tgatnactnc tatngaccag naagaaacta gnaaaancag 480  
 gcagncaccc acctacnenn nctaactatt cnnnnncnna nncnanccaa cctnnnncgg 540  
 natatncnna agaagccaaa ncaagaaaan nagaccnna ngccnaaaaa aaaacngngn 600  
 nancnnaaac atcangaaca ggaaaccagn ngnaaaataa cacagggnat ncaaaagcnn 660

canccggcan nnnnccaaaa acccctaacc anaaaaggcn gncccagaac ccangaaana 720  
 gaaaaccnga aanncccngg nnaancccg cncnncocc caatccacaa ccccccgna 780  
 naancnccn aaaccancc aaaacanaaa acccngnggc naaaaaggcn ccccnaaaaa 840  
 aanggnccc cggnccggcg gncgaacnc cnagggncaa nannggggng nagncaaaaa 900  
 a 901

<210> 199  
 <211> 885  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(885)  
 <223> n is a, g, c or t

<400> 199  
 ttttttnggn ggntttnnnc nnttttnntc nnnnnncccc cccgattnnn nttnngggggg 60  
 aaannnccnn nccanaagnn atnttagnag gaggaataca canttaatat atctcactag 120  
 cattcatttc cctccccac cctcatccca ctccactgct aagagagaga aatttcagca 180  
 ctgctatcct gttttattat acattttocc ttttgagtta aggattttta gattttgaaa 240  
 gtaacagaat agaaacaaa attttnntca acttccaatt tggctnaaaa agagagaaat 300  
 aattattatt tctatgtta cccaaaactt attctgttaa taacagttat nattatatat 360  
 tcaaattaat aaatgaagat cgccaaaatc accttaatat aattgttagc agctaaagaa 420  
 caaaaatttt tttcatttgc ttctataagt agacatcaca tgattacttc tattgaccag 480  
 taagaaacta gtaaatcag gcagtcaccc accattcttt tctaacttc ttttncttat 540  
 tctatncaac ctttnngta tattcttaan aagccaaatc aanaaatnan accttcagc 600  
 ctaaaataaa attgtgntat cttatacatn atgaacagga acctgtngta tataacacaa 660  
 nntatncaa agctttatcn cantttctan aacccttaaa caaaaangca nntcanatt 720  
 nnaanattan aaaactnaat tctggaccca antgtanatt aactctnnan acatttttnn 780  
 gtgnattaan naaaaactgg nnnccatcc ttaactttaa naggtcanc caaanttnn 840  
 nnanaacaan nctnnnnan aancaantta tatnaaacca nctan 885

<210> 200  
 <211> 941  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>



<221> misc\_feature  
 <222> (1)..(941)  
 <223> n is a, g, c or t

<400> 200

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ttttnggggg anntananng nnnnnnnnnn nncnngnnn nnattggggg gaaannnccn      60
nncttngnat ttagaggagg aaaacacntt taatggatct tattagcttc atttcctcc      120
cccacctca tccactcca cngntaagag agagaaattt cagcactgct atcctgtttt      180
atnatacatt ttccpttttg agtnaaggat nntaagattn ngaaagtaac agaanagaaa      240
ccaanntttt ttttcaactg gnaattnggc tcaaaaagag agaaataatt atnatntoct      300
atgttaocca aaactnatcc tgnnaataac agttatnttt atatatcaa attaataaat      360
gaagatcgcc aaaatcacct taatataatn gncagcanan aaagaacaaa aatnctttca      420
nnngcttna ataangnnga catnccatg atcacctnct attgaccagn aagnaacta      480
gnnnnaatna ggchannnac ncacnanann nanncnaanc accannnnna cnaannncna      540
ttcaacannt nannggnana ntnncnnaat aagccnaaat aanananann gccccnana      600
gcctaannan nancgaggna atgcnnnncc caannttnaa caggnatncc nggcagnnt      660
tntaacanng annatttcan angnnnnanc cggnaatact nnnanaannc cnannaaann      720
naaaggnnan tcnnaatnca angttnaana aaangnaatn cncnnnnnnn antantaaat      780
aangncnnna ntannannnn nctancatcn cncncnatgc acnnnnnaaa ntnnnnntn      840
acnnncnnnc nnnngnnaaan nttnaangga nnnnnnnntn ancacannnn cncannaang      900
nnnnnaana nccacaannc aacacatnan caancacnaa t      941

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<210> 201  
 <211> 886  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>

<221> misc\_feature  
 <222> (1)..(886)  
 <223> n is a, g, c or t

<400> 201

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ttttccnng gntnnnnnt nnnnannnn nntccccc catnnnttt ggggggaaa      60
ancacagnaa cacagngttt nngnntcag naaagctttt ttccagtttt gaacgtaaga      120
tatttccttt ttcaccatct cctctatgg gcttccaaat atccctttgc caattccaca      180
agaacagcct tagcgaaagg cttcttgaag ggaaagatgt aactctgtga gatgaattca      240
cagaacacaa agcagttttt ttagaaagct tctttctagt ttgatctga gaatatttcc      300
cttttcacca tagacctcta tgggcttcca aatatcacgt tggaaatttc acaagaacag      360

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tgttagcgaa aagcttcttg agggaaaagc tataactctg tgagatgaat tctacgatac 420  
 atgtaacatt ctacgaacaa ccatgggtgag tagaaccatc tggattttcc atcactttca 480  
 tttaaaagac tctgttgata ttctaggtac tgattccata tatcantatc aacaaatttc 540  
 tcaaccaagg ggataattgg ttnatctgnt tgcaaaantca ttccgtnatt tnanaaaagg 600  
 agagaaaata gctttctntt cancttncca cgcttncct gccaaaaatn ccaanaaaaa 660  
 ancaatngng nngngnggcc ncnntnntg nngnttngng tgnccntgn nctntccnan 720  
 tcccnntnag ggnnaacnaa tttttnnga ctttaanaaa naaaanaaaa aanngncaa 780  
 accacntnn aaactnnttt aaanntncca tnnnaaacct taaancnaa aacaaaaaa 840  
 ancccccacn ancnnnnnnn nanananann nnnccntan ttnttt 886

&lt;210&gt; 202

&lt;211&gt; 925

&lt;212&gt; DNA

&lt;213&gt; Cercopithecus aethiops

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(925)

&lt;223&gt; n is a, g, c or t

&lt;400&gt; 202

ttttntggng gannnctnnt nnnnnnnttn nnecccnct annncttngg ggggaannnn 60  
 cnnocactt agnatTTTT ncncaaaaa aaaaaaatag ccaaagtcct caaacggcc 120  
 tgcattggcac tacattctct ggccctttat cagcactctg acagctctct cctttgctta 180  
 ttttgctcct cattctagcc tctggatctt tgcccttgct gttccttacg ctcttctccc 240  
 agggatctga aanntttttt tccctcacct ccttcagagg tttgctaaaa tgtctctac 300  
 ccagngaagc ctcccccaac caccacatta aaacacaca accntttccc gttctctatc 360  
 ttccttcaact tngcatatgt ccattgngta acatcactta cataccttna attntnagct 420  
 natnaatnca tactncaaaa caccttatnt nttaccatgt nccaagcatt gnccntant 480  
 tgcttnacan tacancncna anatnaaatt cnacanaaaa tcccatnctt tttgaatntt 540  
 tttgaacctt acattngnaa gtncannca aaatccnang ttaaancata aaaatnccn 600  
 tgnanacnna acccctnaaa naaanaaaat angaaganag gggcctgaat tnnngngcnc 660  
 ttccccctcc caaantncan acntectngn angnaaccnn atctnnnnng nntnnnnntc 720  
 actnccgtnt ntcccgaca anaancnccc cnnnccctn ntngccctt ccatnccnat 780  
 tnttnaaana ttaaaanccc ccnncnctn ctaantnct ngggncnct tcaaacctt 840  
 tnaacnaann anncccncc nnaaaaaacn ncnnccnccc tnnngnnccc annnaaatc 900

atccnnentc nntctctnt ctccn

925

<210> 203  
 <211> 895  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(895)  
 <223> n is a, g, c or t

<400> 203  
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 nacgattcan gntttatnnc tacgaacaac cattgtgagt agaaccatct ggatttttnc 120  
 tcactttcat ttaaagact ctgttgatat tctaggtagt gattccatat atcagtatca 180  
 acaaatttct caaccaagg gataattggt ttatctgttt gcaattcatt ccgtaattta 240  
 gaaaggagan anntttcttt cttttcagct tccacgcctt cctgcaaaaa tacaagaaaa 300  
 atcaattgtg tgtgtgtctg tgtctgtgtt tgtgtgtgcn tgtctatgca attcctctag 360  
 ggtaacatat ttttacagac ttaagaagaa aagaaaaatg ttcaaactac attatacttc 420  
 tttaaacatt acatttagaa ctcttaaaact gaaaatcaaa aaacacacac agatctcata 480  
 tgaacataat catgccttat ctatctaagt tctggccttt ctgtgtcttc ggtgatcatt 540  
 actacagagg gaaaggaacc cctgacagat tttccatgtn ttttcatgct tccatacaca 600  
 ttnttctttc accattgaca ccnactanaa aaagaadaccn gtggnccttt ctgagggttt 660  
 ttttttngnn anntnaattn ntttttttta aacttggntt ttccnccetna attnttancn 720  
 taggntnana aaangaaana ntgcctnnna tnaaaanggn nccncaatn ntatnttacn 780  
 cnnanaagnc cnattgggna gggngcanaa antntnanng ggnnacnaaa ataaaannaa 840  
 aaataactct nnnanccttt ggttttacat taacnaaana nntctncccc caana 895

<210> 204  
 <211> 887  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(887)  
 <223> n is a, g, c or t

<400> 204  
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 cnnccacga gnattttttn ctcaaaaaa aaaaaaagc caaagtctc aaaatggcct 120

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gcatggcact acattctctg gccctttatc agcactctga cagctctctc ctttgcttat 180
tttgctcctc attctagcct ctggatcttt gcccttgctg ttccttaacg ctttctccca 240
gggatctgaa aggnnttacac cctcacctcc ttcagagggt tgctaaaatg tcttctaccc 300
agngaagcct tccccaacca ccacattaaa aacacacaac cagcacccgt tctctatctt 360
ccttcacttt gcattngncc attngntaac atcacttaca taccttnaat tnttagttna 420
ttaattcata ctgcaaaaaca acttantttt taccatgtgc caggcattgn ccctagttgc 480
tgacaataca gnnngaaaata aaatagacaa aaateccatc tttingaatct ttngaacctt 540
acattggggag tgacaggcaa aaacgaggna aatcagnaaa atacgtgaga cagaacgcta 600
aaagaaaaaa aagaggaaag ggctganntt ngngncttcc ctccanaatg caagctcctn 660
gagaatacag annngngngn nnnnnacnac ngnatctecn gacaatagcn cccannacan 720
annangcatt ncnacccaan tnnaaaaang annaactnang gcannnnccn aannncnggc 780
cacatnncaa ccntaaaaca anaanacca anaaaaaac ngnnncagcn aggnacacnaa 840
nnaagaaana nccgnncnna attnnngngg caggccntna aanncca 887

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<210> 205
<211> 843
<212> DNA
<213> Cercopithecus aethiops

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<220>
<221> misc_feature
<222> (1)..(843)
<223> n is a, g, c or t

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<400> 205
acccccccca tnnnnttggg ggggaaaaac canccagtaa nagttttggn gcaaggnggg 60
tggtctttaa tcatcagggg caaggtagat ttaattctcc attatccatt aattatttaa 120
tgaacaccaa cagtgggatt gcaagtggga ggtttagaac aacagggctc tgtggcaaag 180
actactagac catgggatca ctagggacag ctagtggggg aggcnttnng ggtattactt 240
ggcttataaa accaaaatag accaacagca gattattaaa atgctggtgt tggtgccaa 300
gtggaacgta ataatcacac atctggtttt ccaaattgaa cagttcttag atccagaatc 360
ctgtgattga tagagatgct agatcctttt gcagaaaatc ttataatgcc ccaatgaatt 420
tatagtagta atttcccaa tcttctcca aaagaatcta tgctgcagaa aataaaatc 480
ctgnacagng ngcattacat tngcactac agagatgaaa gtagccaaat atttcaagtg 540
ctgnngaadc canagttnga gatgacacca ataccagaga aaacaaaaac catcatgatg 600
ccctggntag gnggggtgtg ngaaanccan gnggaaaaan aaagncttgg gcccnacant 660

```

ncanatatataa atgnncaaag agncnggcna cccnccccgn naanaaggnn agggncnctg 720  
 nnggocnaaa nnaggnnngg aagcaccnaa anaannngaa anaaccccc accaaaaacc 780  
 cccngcncn gaccnggana ggggggnncc cntncncann ccaaaanggc ccannggnnn 840  
 ncc 843

<210> 206  
 <211> 927  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(927)  
 <223> n is a, g, c or t

<400> 206  
 ncnccccng gnaancccn ggngtaannn nnncccccc ccaatanntt tgggggggna 60  
 annnccnncn canagtgnaa tantaagnaa ncaaaggcag cngagtcagn accaaaacta 120  
 acagnanaat aacagnaaaa nnnccaccac catatgaaag caggggaaaa atatatggaa 180  
 acagatatgg ccaaaaaaaaaa ggatgcagac aacgaagnaa gcggacagaa gcccgagaag 240  
 aaaaacgggg ncggggggaga aaggagacta tnaataggaa aaangaaaaa gcanacacag 300  
 ggcgactgag caatacagaa agcaaagang cnggataaaa agcagggccc tagagtggga 360  
 gtggcncaac acgaagaggg gcatccagag ggggaataca gcgcngggng acaggagggg 420  
 gnccaaaang gaggaaaagc gcccnncnca gagaaccanc aggcgcggcc cccccgggg 480  
 cggcagccgg ggagggggcc cacagangng ggngagaagc caagaaacnc agcgganggn 540  
 agggaancac nggcccangc gcaggggaca cccccagaa gccnaggaca gagggagggg 600  
 caaggngcac actaagganc cnnnaangaa cggccagagg ngcaggancc cacannagaa 660  
 gnaccngaa ggggcaggng caggcaagnc cccgcngcan gaggacaaaa cnggccngcn 720  
 gaaaanggnc gcccnnccac cccnccngnc cnaaaccac ngcaaccacc agncnnnnac 780  
 annaanccn aaaacacaaa ngccccacn nnanccancc cganaaaaagg cnaanaacca 840  
 ggngnaancc naccacng gncngnanga cccnggaaac cnnnanncca nncnnaannn 900  
 nnaccnnaaa ccaaaagnnc gannacc 927

<210> 207  
 <211> 940  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>

<221> misc\_feature  
 <222> (1)..(940)  
 <223> n is a, g, c or t

<400> 207

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ccccggnatc ntttctgtnt nntnctnnnc cccccctta ttttgggggg ggaannnccn      60
nnnctnnnnn nnnnttncca ccnaaaacta tttnttnnc tnncccgct atcctccaaa      120
ctagcaatan ttcggttctt ccctcttgt ctcgggcgga ttctgaaag tcgtttattc      180
tcttaattaa tacgcgctc cagccccgcc cgttcagctc attctcttaa tcgcattacc      240
ctggctgcng nnnctttttt tttttccac ctgctgccac ccacccagac accgcctnecg      300
gctctttccg gaccatctca gtttctctc cttccccnng cccaattttc tttaggctat      360
ttctggctcc cgtagggttn tcatgctctc gttagcccca ccccatcacc accanccggt      420
ctttttcggc tctctccgn cncctctgt ctcctgctca ggctcttttc cagctattnn      480
cgactccct cntactcacc ctttgcctc ngaaactntc ccacngccc ttcaggcaaa      540
tcngtctcna cccctantc ccgcacgtga acacagncct nccccctccg ctttcttaga      600
nccccctct caccnnnncc ctttccnncc catctcaaaa actananggn tgggtacngg      660
ccnancncc cnttttggtg nnaannccn gaatcgccgn caaggncctg gtnctnccc      720
ngaaaancct atngnccgn cacaacang ggaaacannn ttcncaccn ttntccactg      780
ancncttcc cccntcacc ttnaaanaca tnttttnnt ttatctaaaa ccnttcanc      840
ccnctctct tcgncacct cntnctant ncccatatan cccntagnt natnctnca      900
atnccngcac cnnntntnta tctaathaaa cccaacccc      940

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<210> 208  
 <211> 881  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>

<221> misc\_feature  
 <222> (1)..(881)  
 <223> n is a, g, c or t

<400> 208

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tttttccnng gnnattcnnt gtnnaatntn ntntccccc catnttttg gggggaanac      60
ccgnanttga aatttnggga caaacaaca tanctctttc tctttccttg aagggttaat      120
gctccaacca gcctcagatt ggttcgcttg aatcttaaaa ttacttttct ggtcacgcgc      180
gccgaaggtc taagcatttg tgaaatgtct tttttccccc ccccaacccc ttgatgctgt      240
tctctttggn nttttttaat tacacagggg ttgagaaacc aaattaaaat taggcgtgtc      300
tggtcaacag tgatcacgtt gcatgctttt agctttgntt gttgaagttg cttctctcc      360

```

ctgagtgget ttcttctttt tttttttttt ttttttattt taaaaaggaa atatcataag 420  
 ctptttcaga aatactcaca ggaagtgagt gtccgtatgc tggttactca ccancaactg 480  
 agtggttgca ggtggagaat gctaccgcag ccgcccagac agatctgcag actggcccca 540  
 ttgcagagga ttagacacag ggtgcgtgga tcatagggtt tttgtacaga angcagtttt 600  
 aagaggaaat tgggtcactgc atgtcatctc gaggggtggt gattcangga gccaggcctn 660  
 ggggttcana aagnacgttg ctngccatct tnggaggtt cctgctcact tntcaaang 720  
 ncaggctngc cttttaaaaa tcaatgttcc ttccaacccc aaaagggnnt ctttttgcag 780  
 tgaatcanct nccaaaataa atagccccc n tttttttgga aaagaacgtt tgnaaatccc 840  
 ncnttttaat ggnangtttt naattngggg gttnantcaa a 881

<210> 209  
 <211> 896  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(896)  
 <223> n is a, g, c or t

<400> 209  
 tttttccngg atnttnattt ntanacttat ccccnccatt attttanggg ggnaanccct 60  
 nncanaatat tgtnttacia atatcatttt nggtgatgta tgtcaaaacc aaaactgcct 120  
 ttatgtcaat atgctgtaaa aatctatcag aatatactt aattcttaac tttcattggt 180  
 gtctgtgggt tgtcttgtat aattattatc acatctacag tattttctgt aggtaaatat 240  
 gaaatgtttt tttnatgtac cagggggaaa atgcccttta ataagccttt ccctagacaa 300  
 agcaccattt aggcgttttag aagcaagaac tagtganntc agaaattgct gtcatacata 360  
 ctcacctgtg aatggtcgta caaaggatcc caagcgcagg acttgctctg gaagcagagg 420  
 atcggattcc accaggaaaa gaggaagta gaaatgccaa atgccagcgc tccctttccc 480  
 cagctcatct tattttagg cactcagatt ttggaatcc tccaggacta acaaatanaa 540  
 accacactag gttgtttttc ctaattncct gtgaaatgag tcangtangt caaacanctt 600  
 atccactcca gagagagaac caattccttt gagctacact cctgttttc cagtnaccct 660  
 aatnccctct ntgggtgtccc ttgaanaaag ggnntgccna ccantgcatt ggagagccca 720  
 ccgggtttnt gaatgaagan nattgtnaaa antnnccaaa aagttaannn gccttcaagg 780  
 gganagttn cttttntgaa nattnaagna ggaaaaatcc cannttaaaa tacctgggt 840  
 ccngtttttt nntaaaaaan cnnnnnactt ttttttggn naangntttt tttttt 896

<210> 210  
 <211> 869  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(869)  
 <223> n is a, g, c or t

<400> 210  
 nnccttctaa ttttntagtt tnnnagctca cttataaanc aggctacagt gttattctta 60  
 agtattcatt gttgtataac acactacccc caaaatttag gagcttaaaa taacagcaaa 120  
 cacttattat ctctcatggt tctgtgtggt gactagacat ttcggctcct gtgcagatgg 180  
 ctggagcact gagctntttt ttnggtctac agtgcctcgc cttacatagt aggcaactagt 240  
 gttggctgct ggtagcaagc tcagttgggt gtgttgacca gannnnttgg ttctgctcta 300  
 gagcattgta atantgagca tttcaacagt attaacccaa catgcaaaca ctactatag 420  
 taagcaaaat aaaataaaat aaagcccccc cccagatatc tatgctctaa aacttccaaa 480  
 cgtatgaata tgtnacctta aatagcaaaa ggcactntgc agtgtgattn angcaagatg 540  
 gggcagagtg tctgggaata tccangtgga acccaataat gcaaataaaa aaaatcnttt 600  
 tataanangg naggtaggaa ntaanacatc tgntcancat taccgctgcc nggtttttng 660  
 aaaaanaaaa ttnggaagaa aggggccnca agccaaggga atnccaggga tttcnctaan 720  
 tnggccaaaa caanannatn aaaantcntc ccccnnnnnc cnncnanaaa aaantgnaac 780  
 cctgggcgnc cncnttgatt tttnnnccca angancctnc ctnaccaana nantnaaaaa 840  
 aaaatctntt gntcgnnttt nancnaaan 869

<210> 211  
 <211> 874  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(874)  
 <223> n is a, g, c or t

<400> 211  
 tttttngggg atttcccttn tanantnnan cccccccctt anttgggggg gaaatacnnc 60  
 ccattaacag ttttactcgc agcctctgct tngtctacat ctgctgcaa cttttaacta 120  
 atggcgagat actttcgcta tttccgatgc cattaggaaa caaatagaaa aatagtttgg 180



caacaacatc ttctcgaata ttatcacttg acaaatttta acgttttagg tggaaacgga 240  
 attttaannt tttgttttaa gaagcttaaa aaaaacaggc atgcttaatt agcataatgc 300  
 tgaatggcag ccaatcacia actgaatttt taaagcnnga agtgtttgct cctggcggtg 360  
 cgcgcccgcc tgtaatccgg gaatcccagc gttttgcgag cccacgceca ggccgaggag 420  
 ggaggatcct ttgttccacg agttcgacac cagcctaggc aatatagcag aattcagttc 480  
 aatgactcta ggcttttagcc atgcagtatt aacaaatggg atattaacaa tattaacaaa 540  
 tgggataaaa accaagaact tgacaaatgt gtaatttcc tatttctgtt ttaatacatt 600  
 acacaaaact aactgcctga aaacaaaaca aaagntntta tttttatagt tctctaaatc 660  
 agaanttttc attggggcnt aaaatcaagg tnnctcgcaa ggctgcattc tttntgnagg 720  
 ctgtagggga naaatttcat tgtccttgnt ngncctttaa naaagcctgt tttnccttgg 780  
 cttggngncc cctttttcaa ttcattttta aaaccccnan nnnatnngnn ccnnttctn 840  
 cctecnectc cncnttaaaa nattttttnt gngn 874

<210> 212

<211> 866

<212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc\_feature

<222> (1)..(866)

<223> n is a, g, c or t

<400> 212

annnnnnnnn nnnnnnnncc ccngatann ttggggggga aannncnca tttgagtgt 60  
 ncaggggcaa accaacagta aaccagacta ctaaagattt acttggtgaa tttttttgca 120  
 aagtgtcaaa gggtttatag agaaaatgaa acagttcttt aaagatgttc ttgagcgagg 180  
 tttttttttt ttttaacttac taaaagactt tatgttttag aacagttttt gtttacgttn 240  
 agcacgtagg acgtcccccac tacacacaca gnttctctta ttaatagata ttagtatggt 300  
 acattngntg caactaatga accagtaatg ataaattatt aactaagatc catagtnnat 360  
 tctgtcttcc tcacattnta tctaaagncc tttntctgnt ccaggatccc agctaggaga 420  
 tngaaagacc ccacctgnag gttnnggaag ctagctgagg atcgnnnccg atgatngaac 480  
 aagatggatn gcacgctggn tctccggccg ctngggngga gaggctatnc ggctatgact 540  
 gggcacaaca gacaancggc tgctctgatg ccgccngnnn ccggctgnca gegcaggggc 600  
 gcccggnncn tttnggnaan accgaccngn ccgnggccn gaangaacng caggacnagg 660  
 canngcggnn atcngngntg gccacgacgg gcgnnccnng cgcannnggg cncnacgnng 720

nnacngaaac gggaagggnna -ccggcngnna nngggncaaa angccggggc aggaaccncn 780  
 gnaannaaa ccnggnnccn gccnnnaang aaccanaang ggngnnnnaa agnggggggn 840  
 ngnananccc ngnaaccggn ncccc 866

<210> 213  
 <211> 998  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(998)  
 <223> n is a, g, c or t

<400> 213  
 ttccgggggtc tanaangtnt nntnntncan ncccccccn tttttggggg gnaannncnn 760  
 nccagtttnn natttggnnn nggagcataa attnagtcgn ctctctcacc taaaactcat 120  
 ggtctggtgg aggctccgcc tcctttgtcc cctttcatgt ttctgtctca gcatgectgg 180  
 cbccttaagg ntcttcatct ttgacaggt tatctcaagn ctcaattgaa ccgccncctc 240  
 ctgncaggcn tttttnnct gggaggtgag cagnnggggc cggaatgtg ggagctaagg 300  
 gcatagatgt gaggaccncc ctatgaanag gaaaaggann cncctggaat gcanacctgg 360  
 gactgtctgt atacctgcct ggtcactaaa ttctcttgag aggcataaac agnnaaaanc 420  
 ctganagggt tatngccaag agcatngatg gggctctgctt tctggganc aggggaataaa 480  
 ggnngtgata cccanaggga ttatntctca gccaggncct tccttcccnt gtangannag 540  
 tcccttgagc cncnncna ctanancntn ttttnaatna aacnccctn tnnncgggac 600  
 aacgggaann tccctatann cctccannc tnggttgnnn aanncccggn gctaaaagca 660  
 atcnncntn nccntnggtc tncacaaaan ggctnagaat naccangttg nagecccntn 720  
 ntncctant cccccctgna nnnctatnat ttnttccaan taaccaatna nccccccan 780  
 aaccannat acanacaac atngacccc ntcaaaacca acanccnnnt agacntntn 840  
 ocnacntnnt aggnatng cnaaccgnaa gcntttgttn tngaantn ccaagggcct 900  
 cncnaacaan ttcaaaaana agtgggtgntt ccccccncct naaccccgng ccccccacnt 960  
 caacanant aaaaannaan acccacncc nntngtng 998

<210> 214  
 <211> 956  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(956)  
 <223> n is a, g, c or t

<400> 214  
 ttttttcggn ggattnctnn tttntttnt tnncccccc ngtnnttgg gggggaannc 60  
 cancgttctn nctatttctt tcttgacgag ttnttctgag cgggactctg gggttcnaaa 120  
 tgagctagcc cttaagtaac gccattttgc aaggcatgga aaaatacata actgagaata 180  
 gaaaagtca gatcgaggtc aggaacagat ggaacagggt cgaccggctg accggctcgac 240  
 cctagagaac nnttttntgt ttccagggtg cccaaggac ctgaaatgac cctgtgcctt 300  
 atttgaacta accaatcagt tcgcttctcg cttctgttct ntcgcttctg ctccccgagc 360  
 tcaataaaaag agcccacaac cctcactcg gggcgccagt cctccgattg actgagtcgc 420  
 cgggttacc gtgtatccaa taaacctct tgcagttgca tccgacttgt ggtctcgctg 480  
 ttccttggga gggctctctc tgagtgattg actaccctgc agcggggggc tttcaatctg 540  
 attgcctctt gcttgacggc aaggagtccc gaccactgaa cactgatgac ctcatctggt 600  
 gtgattgtct cttgcttgac ggcgaggagc cccgacgact gaacatggat agtcgccgcc 660  
 acagcacggt gatcanaagg ctttcgttcg acttatgant ccgacgntcc ggggagttca 720  
 aagccccctt tcnactcctt gggncctttt ngtnnttntc ttgnccacct ttcttgactt 840  
 cttnaanttt gcttctggan tgntaatnch natchnaaan ccttgtttgn aaaancntgg 900  
 ccccgngncc cngnttcntt nccccann tantgnttta ngncctntt tggaaa 956

<210> 215  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(915)  
 <223> n is a, g, c or t

<400> 215  
 ccncaacctt ngagacccta aagacattgg agcagcccca tacacctctt cccagggcac 60  
 acaaaggccc ctgacatgcc catggcagtc caaggcctcc aattggagcc atctttggta 120  
 aatctggggc ccatcagccc cactgcccct tcttgggtacc ctgagcatgc tggcaagggg 180  
 actnnttttt gcaccccatc ttgtntcata taccacagn acctgatgtg gacatgactc 240  
 accctggggc cctgtgagtc aataaggggt tntgantaag gggcagagca tttcaactta 300  
 gtcccataac ccatgagctc attaagcaaa tattacccat gcctagattt ggggccagtc 360

actaccact ggaggctgtg ggctccaagg tatggcagca ggggaggoca gccaggcntc 420  
 tggccagctc acccttccct gtgaggatgg acnccagcca ggctccac ctccaccct 480  
 agactggggg acccggtt ggggggcaag aaaggggacc tgaaagtggg tgtctnggag 540  
 ntaagcccat ttcttnata ctccnccaat aggganccaa gaaggngggg tnagagttac 600  
 cccaanaact caccccaacc cantntnaac gctgtggggg ctcaangggg acangcnaaa 660  
 acnaaaantn anacngggcc aaaaaagaac aggtncggnc ctncoccnan ggaccttttn 720  
 ttttctaeca ccttaccan nanaatnctt gaccaggggc ntttcccaa acncngnaaa 780  
 anctttcaag cntngnact nttnanacc ngggcnnnnn aaggnttagg gcctcttnnn 840  
 ancnctntgn cnggttncca tngnntaaaa accccaangn aactccteca aanaacaagn 900  
 ancnntctn ggttn 915

<210> 216  
 <211> 949  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(949)  
 <223> n is a, g, c or t

<400> 216  
 tttnncnggg nanntttntg nggaannctt nncnnccccg gnttttttgg ggggnaannc 60  
 ncatcgttct tactattgcc ttcttgacga gttnttctga ggggactct ggggttcgaa 120  
 atgagctagc ccttaagtaa cgccattttg caaggcatgg aaaaatacat aactgagaat 180  
 agaaaagttc agatcgaggt caggaacaga tggnacaggg tcgaccgggc gaccggtcga 240  
 ccctagagaa cctttntatg ttccagggt gcccgaagga cctgaaatga ccctgtgcct 300  
 tatttgaact aaccaatcnn ttcgcttctc gcttctgttc ncgcgcttct gctcccgag 360  
 ctcaataaaa gagcccacaa cccctcactc ggggcgccag tctccgatt gactgagtcg 420  
 ccgggtacc cgtgtatcca ataaaccctc ttgcagttgc atccgacttg tggctctgct 480  
 gttccttggg agggctctct ctgagtgatt gactaccga gtggggaacg ggggcagggc 540  
 ggggtggagg agggcgagg aggtgagac agccagggtg agagagggcc aagcttgaaa 600  
 ggttttccca ggcttgggga gaggccctgg tcaggatgtg tatgggtaag gggtgagaga 660  
 cagaggtncn tggggcangc ccggacctgt tttttngnc cagtntcagt tctgnttcnc 720  
 ttgnccctga gaccacagc tcanagaggg ttggnncggt tnggggnga cnnttanccc 780  
 catctgatcc catggtggnn ntganganan gggctaannc nancnctn cagtccttn 840

ttgcccncac tccgggcccac atcnnngnga agagggagac cgcctcgnccc nccccagga 900  
 agggnnncngg nanaccgggn gnccccgnng caaccngnaa ccaacnnan 949

<210> 217  
 <211> 999  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(999)  
 <223> n is a, g, c or t

<400> 217  
 ttttcccngg gannnnnntg nnnntttnnn nttcccccc cocatnnnac attggggggg 60  
 aaatncccc catntagcc tttngcnaa agaccagtn ntctgcccct gggtncnc 120  
 agganctctg caatggggaa gtgagccctc ctgaggcctg gctggcagga ggctctcaa 180  
 ggtcatgtgg acttccccca acacctcgag tttctgcaca gcagccacgg agacgggcct 240  
 gggggctggc gggaaatatt tnnnaaggca atgtttncct gagtgggctg aaacctgaga 300  
 tgaggaaatg agaagacgtc aggtggctgg aggacacggg cttaggaca gccagcacc 360  
 agccctgtag ctgaggcctc cggagggagc cagagggaaa gggagtccc tccccgcggc 420  
 ctgagtctct gccagtgcc agcactcca aaggatccac cccaacctga gagacctaa 480  
 agacattgga gcagccccag acacctcctc ccagggccac aaaggcccct gacatgcca 540  
 tggcagtcca aggcctncaa ttggagccat cttttggtaa atctggggcc catcagcccc 600  
 cactgncct tcttggtacc ctgagcatgc tggcaagggg actggaaact gcatcccatc 660  
 ttgtctcana taccacagn acctgatgtg ggacatgact caccctgggg tctgtgagt 720  
 caataagggg gtttgantaa ngggcagaac nnttnaactt antnccanaa accatgagc 780  
 tcattaannc aaanttacc tgcctanaat nggggccant nactaccnac tggaggttg 840  
 tggcttcang natggtnag ggaagnecc nggctttccc aannnnnct tncctngag 900  
 gnggaccac cagcctccan ccccccnna actgggaacc nngngnggca anaagggcng 960  
 aaanggtttt gantaaccna tttntanncc cngggnaaa 999

<210> 218  
 <211> 962  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(962)

<223> n is a, g, c or t

<400> 218

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nnnncccggn actttcnnt anngnanncc cccocctnat ttgggggggna annacannnn 60
ttannnattt nnnnnngaca aagctttttt ccagggmntg aacngcngga tatttcctnn 120
ancaccatag ccgncatagg gcttccaaat atccctttgc catttccaca agaactgcct 180
tatcgaaagg ctctctgaag ggaaagatgt aactctgnga gatgaatnct ccagaggaat 240
cctggatnnt nnccataggn angnctnaac ctgttctact cngancttng ggaggggtgca 300
cctggaagca agctctgggg tccctggggag agaaagcaca gcccctgccc tggagacact 360
caaagcctgg aaggggaaggg cagngggctg gacagagacc acaggtgtga cggctcctagg 420
tgggaggtgg gagctcagag ggggcaccta accccattgg gcagagtgtc canggaaggg 480
tttgagtagc gccncagagg atgcngnaga ananccccag gaggagagcg acngnatgna 540
gaggggaanag catttaccgn ngcctggggag tnggagaggg ctggcngggag aaaaagagc 600
tccangaagc cacaaancct cannagnngc gtccacagcn cgatnctna ncaccnaca 660
cananccccg ccncatanaa agngcnccaa nccatcnntc acngaangaa nnaacaaaat 720
gaaanaaggg agatcaccna agggaganac gcngacaccc ccccnccccn accnganaac 780
cacnncanaa cntnnacccc gcanaccnaa ganccatgaa ganttnagca cggngangcc 840
cannnaaaag ncataaanan aacngnagga aaagggaccg gacaccnnaa tnaactcccc 900
cacnntacc caaaaccaca ncnncngccn gggcgnaatn cccnacnacc aaccancccc 960

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<210> 219

<211> 891

<212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc\_feature

<222> (1)..(891)

<223> n is a, g, c or t

<400> 219

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tttttngggg nttnnnnggg gnnngnnnt cccgcctnnc cttnngggggn annctnnnc 60
agttgggaat tnatttaaag aagggaacta agggagatta ttaaagagcc agnaacgcaa 120
aggagagctg cggcaatcga caactaccga agacgcgaag cacattcacg aagcggtccc 180
ttcaatccgc aactacact cccacgaccc gccccttcg cccacagagc ccgccacttc 240
cgctcanan ntnacgccc ctctgtgtc ctaagggcct tccgcgggt gatcagagcg 300
cccgcctt agccgcaaca gaagccgtaa agctttctcc cgtcgcgatg cagcgctcaa 360

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ggcgccctgcg cagaccctga aaagcggcca gggcggcccc gagctccct tttccggttg 420
cagcgccgcg cggtaggtt ctctcgttct cgctcgcagc catgccgtcc aaggccccgc 480
tgacgtcggg gcaggtcttc ggacgcaagg tgagctagac gccagatggg aaggggaggg 540
gaaggagaag gtcaggggtc gggagaggac ggtgggcagg aatacagggg gcaacatggg 600
agctggatcc cgagctcacg gggccacact ctcttgatc ccacagaaga cagccacagc 660
tgtggcgcac tgcaaacgcg gcaatgggtc catcaagggt aacgggcggc ccctggagat 720
gattgagccn cgcacgctnc aatacaaggt gnttggcatt gggncattcg ncgttgantt 780
ggattggagg acctntngga nataatagta gctnnttgaa agcttgaggg ggcnggntnt 840
cancanccgg gnttttnana antngnttn gtntnnnnaa aaggggggtt t 891

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&lt;210&gt; 220

&lt;211&gt; 902

&lt;212&gt; DNA

&lt;213&gt; Cercopithecus aethiops

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(902)

&lt;223&gt; n is a, g, c or t

&lt;400&gt; 220

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tttttnnngg nntataattt ganntatnta tccncccat aaaccttggg ggggaanaca 60
aggncтнаag ttttttagga ttgtgctact gtactccagg gtgagtгaca gcaagtatac 120
tgttcttaaa aaaagaacct tatatattaa aaaaaaattt ttttttaact gaccctgcaa 180
tgacacatatg cttcctttta aaagtagtaa acttcagaag gggcagaaat cagactctgg 240
tttctttcca ttttnagcca aagaaactga nagtnccaaa cagggaacag aagaaccctt 300
ttcacaagca agcatttaaa cagacccaaa ttcggccgcg cggctcacca ggctggctag 360
gagttctaga ccagcctggc cgacatgggt aaaccacgtc tctcctgaaa atacaaacat 420
tagccggccg tgggtgggtg cgccctatagt cccagccacc cgggaggctg aggcaagaga 480
attgcttgaa cccggagggt ggaggttgca gcgatccgag atcgtgccac tgcactctcc 540
agcctgggcg acagagcgag actccctctc aaacaaataa atngaaaaaa aaataaacag 600
acccaaattc aagctatttc aatacttact gagcacttac aatgtctaaa acgctgcttt 660
tagacgcctt ggggttttnt taaggatnaa aacacttgnt ncttngtgaa aatnaaanct 720
atgaaaactg ggtgttcctt caanccttn gggntcccc cggnttccc cnnttnaat 780
gaaccttnt aaacattncc aattttnaaa agncancccc nntaatntt taanaenccc 840
ccaatttnaa nnttttaaan ttttntnaa acnntaaanc cccgggtttt ttttnnnaa 900

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aa

<210> 221  
 <211> 907  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
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 <222> (1)..(907)  
 <223> n is a, g, c or t

<400> 221  
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 tcgccttcggt ggtccgacat ggtgaccgga tttagagacg ctaaagcaga gacaatcgaa 120  
 gaaaagctgg agaacctcta tctggttctg gtttgtggaa gctccgtctc ttagcaaccg 180  
 cgagacgann ttttcagcga tttccggttc cgteoctgtc tggcaagggc ccggattctg 240  
 ggtgcaacct gccggcgtgc gcgtgcgcca gttctntnnn gcaccggggc ggagagtgat 300  
 gagtgcgtgg ctggcggctg agctccttag tgtttgctgt tgcacgctcc ttcgggtctc 360  
 tctggagtta ctgcgtgaaa aggctgcctt gtaagacagc caagaaaaca ggaagagggt 420  
 tggaggcaaa gtccnaata gggattgaaa gaccocacct gtnggttttg gcaagctagc 480  
 tgaggatcgt tcgcatgatt gaacaagatg gattgcacgc tggtttcttc ggccgcttgg 540  
 gtggagaggc tatttcggct atgactgggc acacagacat tcggctnctt ttantgccnc 600  
 cngngtncng gctgtnagcg naggggacgn cccgggttct ttnttgnaaa gaccnaccg 660  
 ttccgggtgcc cttaatnaan ctgnanggac gagnnnancc cngntttatt ttgntgggcn 720  
 ncaacggncn ttccttnnac anctngntcn ncancnttgt nanttaaccn gnaanggnnc 780  
 tngntngttt tggncnaaat annccgggca aggaactccn nnnnannccc ccgtgtnnnt 840  
 nccccaaan tateatng ggtancnaan cngggnnnnn tnaccnnnac ccgnnnnccg 900  
 ccnanc 907

<210> 222  
 <211> 955  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(955)  
 <223> n is a, g, c or t

<400> 222  
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 tggctgtctt acaaggcagc cttttcacgc agtaactcca gagagaaccg aaggagcgtg 180  
 caacagcaaa cactaaggag ctacagccgc agccacgcac tcabcaactct cgggcccggt 240  
 ggcgggcaga actggcgcac nnttnnnccg gcaggttgca cccagaatcc gggcccttgc 300  
 cagacaggga cggaaccgga aatcgctgta cgtctcgtct caggttgct aagagacgga 360  
 gcttcacaaa accagaacca gatagaggtt ctccagcttt tcttcgattg tctctgcttt 420  
 agcgtctcta aatccggtca ccatgtcgga ccccggaagg gagacctgc gaagcacctt 480  
 tccctcttac atggcggaag gcgagcggct ctacctgtgc ggagaattct gtgtgaaatt 540  
 gttatccgct cacaattccc acacaacatg agcgtcagac cccgaagaaa agatcaaagg 600  
 atcttctttg agatcccttt ttttctgcgc gtaatctgct gcttgcaaac aaaaaacca 660  
 ccgntaccag cggnggtttt gnttngccg atcaagagnt accaaantnt ttttctnnaa 720  
 gnaacttggc tttagcnaaa ccnaaanacc aaatactgnc ntttngngta cccgtantta 780  
 ggccccccct taaaaanttn nnancncta atancngtt ttntaatttn ttacaanggg 840  
 tnttgcnaagg gnaaaaattn gttttaccgg ttgncnnaaa aaaattttcc gaaaggcccn 900  
 ngtnngntaa aggggntctg cccaacccat tgggnnannt ccnccannt naatc 955

<210> 223  
 <211> 927  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(927)  
 <223> n is a, g, c or t

<400> 223  
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 cntatcatnn cccatcactg ggtaatatc acagnatcaa attatcctcc ctaaccagct 120  
 cctgtgaata ttctcattga tctcaaaact cactttggcc tcagtgatcc ccaacagcct 180  
 cctttacaac cttacaacat ccaagttcct gttctgtgag agtttctct cgaacacaaa 240  
 cattccgtac aattcagct ctactccgt caatcctcta cattggcagt gagaccttat 300  
 tttgtgaccc ttactttac agcagccatt tcaaagagac attctctagc ctgaaagggc 360  
 tccagattct ttcaactttc tattatgtat gcattgocaa tattgaattt gcactatctt 420  
 atcaactatt ctaaaactac tgacatttgc agaaactggt catttgttct tagggaaaat 480  
 gtctgtgtta tccaaaaatg gagattaaaa acttgcacac attcctactt gatttcacaa 540

gngacctgat ctatggtatc tagcttcctt cccctctgcc ccaagttcac atttccatca 600  
 gctcatatat actcttccct ttctactcct gctgacaggg tccaaggata ctgectcaaa 660  
 aactctataa aaganaataa aaactnatta actggctttn ctatcnaaaa nctttcnact 720  
 agnaatatta ahaaangntt ttcaaccggt nggatccgaa ancatccnaa gnagggnatna 780  
 ngccnaaaaa aaaaataatn nntttcccn aaaaannaaa aaatagnntn tnangggggc 840  
 ccngnncntn gnaaaagaaa naannccggn cntnnaaaana nnannaaaaa nntccncngg 900  
 nttannnnnn aaaaancatn aancnnn 927

<210> 224  
 <211> 936  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(936)  
 <223> n is a, g, c or t

<400> 224  
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 cccccacag nncacttcg cggtgccag gcagtcaggc aaagnaggcc gaagcaaagc 120  
 cctagaagca aagccacagg aataagtcag ctttcccaga ggtcaaagaa ggctgtaggg 180  
 ccacctgcc cgcctccga ccccgccgc gcggcctggg ccgctcccc aaccaaagag 240  
 gccgaattc agagannttt tagcagtttc acagaaagct tcttccagt ttgaacgga 300  
 agatatttcc ttttccaccg taggcctcta tgggcttcca aatatccctt tgccaattcc 360  
 acaagaacag ccttagcgaa aggcttcttg aagggaaga tgtaactctg tgaaatgaat 420  
 tctgcttata ggtcttgaga taaagtcacc gatctcatat catggattat aaggttttcc 480  
 ttctattttc tggcattttg gatatgtaat gatgagcatc agaaagtta atcatattta 540  
 atttttagaa ttattaaata ctctgaggt cattttgggt gatatttngt ggctttcaac 600  
 cataaagaga tcaatgcctt gcagatataa agctttcctt ttccttcttt aataattnta 660  
 aactctgaat tnatgnctac agatatntaa tngatcataa atganaaatg ngatactatt 720  
 cnetacctcc ttatctgttc tcggaanaga ctatacanc ctcgaannat ngaagttnan 780  
 gattgcttnt acgaaannna aaaaaaatn acttnttttt nggcaanana aaatgcttcc 840  
 tccgttgna actccctca ngngtntta gggggnannc taccttnaan ttcctngnc 900  
 ctggnnncng tnnnaggan tgcaaanngn tttctt 936

<210> 225  
 <211> 605  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(605)  
 <223> n is a, g, c or t

<400> 225  
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 tagnaaaaat aatantgtac aagattttat ttttgtcttt aaccagaatg atgtatttgg 120  
 ttaagaagat agtccaagtt aaaggcatac attcaagcta gtggcacatt cggaagagca 180  
 gacaaagata gttggttgca aatgggaaat ttaagccatg atcttaaaag gacagaatgg 240  
 atatttgtta cttttnctat gggaataatt gatttttttc acctccctt tcttggattt 300  
 tttttttttt ttaaattagt ttggttactt taaccttact gtcggttata ttggttctct 360  
 ttttatgtct gagttttttt ttttttttga gacggagtct tgctctgtcg ccaggtgg 420  
 agtgcagtgg ccggatctca gctcactgca agctctgctt cccgggttta caccattctc 480  
 ctgcctcagc ctncctgagta gctaggacta caggcgcccg ccacctngcc cggttagttt 540  
 tttgtatttt ttagtagaga cgggttttna ccnnntnnn ncanatggtt tnnntctnct 600  
 ntctt 605

<210> 226  
 <211> 654  
 <212> DNA  
 <213> Cercopithecus aethiops

<220>  
 <221> misc\_feature  
 <222> (1)..(654)  
 <223> n is a, g, c or t

<400> 226  
 tttntngggg nnnnnnnngn attgnnnntc cccccgtnn nttggggggn aannccnncc 60  
 antactgttt gaggaagac tgaggntcag atggcagagg ctccntagag gaaggaggct 120  
 acagccttga gggcatcagc tttccacact cccaacctgc tgctctctc tgctggaatg 180  
 aggagggggc tcctggctgg ggtctccag ggtggaggga ggagctcaca ttcttagcat 240  
 tcctntncc ctgagttgca aggaagacct ggtgagcatg ctgacccag aggagtgact 300  
 caggcccatg gctcgagtgc ctgaggagg accagggtcg gggatggggc atgagtcagc 360  
 ctggcaggtc ccataagaag ggaagggaag ggagagaaat gggggctgca caggtgtgag 420

ggtctgtgca tgtctgtgtg gtgtggtggg gtgtctggat atccgngtgt tctggatctg 480  
 agtgttagtg tatccgncag cacaacctct gtgtgagggg gtgtctnggc gaggggtgggc 540  
 ttctgtggat gtcccntgtg tggnatgtgt gngtgtgtgt gtgngngact aanntatnnc 600  
 cttcaacnng ggntctnncc caangngnnt ntggatctnc atannatgtc tctc 654

<210> 227  
 <211> 2635  
 <212> DNA  
 <213> homo sapiens

<220>  
 <221> CDS  
 <222> (285)..(1679)

<400> 227  
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 gaggggtggcg agggggcgcc aggaccgca gccccggggc cgggccggtc cggaccgcca 120  
 gggagggcag gtcagtgggc agatcgcgct cgcgggatcc aatctctgcc cgctctgata 180  
 acagtccctt tccctggcgc tcacttcgtg cctggcacc ggctgggcgc ctcaagaccg 240  
 ttgtctcttc gatcgcttct ttggacttgg cgaccatttc agag atg tct tcc aga 296  
 Met Ser Ser Arg  
 1  
 agt acc aaa gat tta att aaa agt aag tgg gga tgc aag cct agt aac 344  
 Ser Thr Lys Asp Leu Ile Lys Ser Lys Trp Gly Ser Lys Pro Ser Asn  
 5 10 15 20  
 tcc aaa tcc gaa act aca tta gaa aaa tta aag gga gaa att gca cac 392  
 Ser Lys Ser Glu Thr Thr Leu Glu Lys Leu Lys Gly Glu Ile Ala His  
 25 30 35  
 tta aag aca tca gtg gat gaa atc aca agt ggg aaa gga aag ctg act 440  
 Leu Lys Thr Ser Val Asp Glu Ile Thr Ser Gly Lys Gly Lys Leu Thr  
 40 45 50  
 gat aaa gag aga cac aga ctt ttg gag aaa att cga gtc ctt gag gct 488  
 Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg Val Leu Glu Ala  
 55 60 65  
 gag aag gag aag aat gct tat caa ctc aca gag aag gac aaa gaa ata 536  
 Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys Asp Lys Glu Ile  
 70 75 80  
 cag cga ctg aga gac caa ctg aag gcc aga tat agt act acc gca ttg 584  
 Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser Thr Thr Ala Leu  
 85 90 95 100  
 ctt gaa cag ctg gaa gag aca acg aga gaa gga gaa agg agg gag cag 632  
 Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu Arg Arg Glu Gln  
 105 110 115  
 gtg ttg aaa gcc tta tct gaa gag aca gac gta ttg aaa caa cag ttg 680

Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu Lys Gln Gln Leu	
120 125 130	
tct gct gca acc tca cga att gct gaa ctt gaa agc aaa acc aat aca	728
Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser Lys Thr Asn Thr	
135 140 145	
ctc cgt tta tca cag act gtg gct cca aac tgc ttc aac tca tca ata	776
Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe Asn Ser Ser Ile	
150 155 160	
aat aat att cat gaa atg gaa ata cag ctg aaa gat gct ctg gag aaa	824
Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp Ala Leu Glu Lys	
165 170 175 180	
aat cag cag tgg ctc gtg tat gat cag cag cgg gaa gtc tat gta aaa	872
Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu Val Tyr Val Lys	
185 190 195	
gga ctt tta gca aag atc ttt gag ttg gaa aag aaa acg gaa aca gct	920
Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys Thr Glu Thr Ala	
200 205 210	
gct cat tca ctc cca cag cag aca aaa aag cct gaa tca gaa ggt tat	968
Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu Ser Glu Gly Tyr	
215 220 225	
ctt caa gaa gag aag cag aaa tgt tac aac gat ctc ttg gca agt gca	1016
Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu Leu Ala Ser Ala	
230 235 240	
aaa aaa gat ctt gag gtt gaa cga caa acc ata act cag ctg agt ttt	1064
Lys Lys Asp Leu Glu Val Glu Arg Gln Thr Ile Thr Gln Leu Ser Phe	
245 250 255 260	
gaa ctg agt gaa ttt cga aga aaa tat gaa gaa acc caa aaa gaa gtt	1112
Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr Gln Lys Glu Val	
265 270 275	
cac aat tta aat cag ctg ttg tat tca caa aga agg gca gat gtg caa	1160
His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg Ala Asp Val Gln	
280 285 290	
cat ctg gaa gat gat agg cat aaa aca gag aag ata caa aaa ctc agg	1208
His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile Gln Lys Leu Arg	
295 300 305	
gaa gag aat gat att gct agg gga aaa ctt gaa gaa gag aag aag aga	1256
Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu Glu Lys Lys Arg	
310 315 320	
tcc gaa gag ctc tta tct cag gtc cag ttt ctt tac aca tct ctg cta	1304
Ser Glu Glu Leu Leu Ser Gln Val Gln Phe Leu Tyr Thr Ser Leu Leu	
325 330 335 340	
aag cag caa gaa gaa caa aca agg gta gct ctg ttg gaa caa cag atg	1352
Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu Glu Gln Gln Met	
345 350 355	
cag gca tgt act tta gac ttt gaa aat gaa aaa ctc gac cgt caa cat	1400
Gln Ala Cys Thr Leu Asp Phe Glu Asn Glu Lys Leu Asp Arg Gln His	

360	365	370	
gtg cag cat caa ttg ctt gta att ctt aag gag ctc cga aaa gca aga			1448
Val Gln His Gln Leu Leu Val Ile Leu Lys Glu Leu Arg Lys Ala Arg			
375	380	385	
aat caa ata aca cag ttg gaa tcc ttg aaa cag ctt cat gag ttt gcc			1496
Asn Gln Ile Thr Gln Leu Glu Ser Leu Lys Gln Leu His Glu Phe Ala			
390	395	400	
atc aca gag cca tta gtc act ttc caa gga gag act gaa aac aga gaa			1544
Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr Glu Asn Arg Glu			
405	410	415	420
aaa gtt gcc gcc tca cca aaa agt ccc act gct gca ctc aat gaa agc			1592
Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala Leu Asn Glu Ser			
425	430	435	
ctg gtg gaa tgt ccc aag tgc aat ata cag tat cca gcc act gag cat			1640
Leu Val Glu Cys Pro Lys Cys Asn Ile Gln Tyr Pro Ala Thr Glu His			
440	445	450	
cgc gat ctg ctt gtc cat gtg gaa tac tgt tca aag tag caaaataagt			1689
Arg Asp Leu Leu Val His Val Glu Tyr Cys Ser Lys			
455	460		
atttgttttg atattaaaag attcaatact gtattttctg ttagcttggtg ggcattttga			1749
attatatatt tcacattttg cataaaactg cctatctacc tttgacactc cagcatgcta			1809
gtgaatcatg tatcttttag gctgctgtgc atttctcttg gcagtgatac ctccctgaca			1869
tggttcatca tcaggctgca atgacagaat gtggtgagca gcgtctactg agactactaa			1929
cattttgcac tgtcaaaata cttggtgagg aaaagatagc tcaggttatt gctaattgggt			1989
taatgcacca gcaagcaaaa tattttatgt tttgggggtt tgaaaaatca aagataatta			2049
accaaggatc ttaactgtgt tcgcattttt tatccaagca cttagaaaac ctacaatcct			2109
aattttgatg tccattgtta agagggtgtg atagatacta tttttttttt catattgtat			2169
agcgggttatt agaaaagttg gggattttct tgatctttat tgctgcttac cattgaaact			2229
taaccagct gtgttcccca actctgttct gcgcacgaaa cagtatctgt ttgaggcata			2289
atcttaagtg gccacacaca atgttttctc ttatgttatc tggcagtaac tgtaacttga			2349
attacattag cacattctgc ttagctaaaa ttgttaaaat aaactttaat aaaccatgt			2409
agccctctca ttgattgac agtatttttag ttatttttgg cattcttaaa gctgggcaat			2469
gtaatgatca gatctttgtt tgtctgaaca ggtattttta tacatgcttt ttgtaaacca			2529
aaaactttta aattttcttca ggttttctaa catgcttacc actgggctac tgtaaatgag			2589
aaaagaataa aattatttaa tgttttaaaa aaaaaaaaaa aaaaaa			2635

&lt;210&gt; 228

&lt;211&gt; 464

<212> PRT  
 <213> homo sapiens

<400> 228

Met Ser Ser Arg Ser Thr Lys Asp Leu Ile Lys Ser Lys Trp Gly Ser  
 1 5 10 15

Lys Pro Ser Asn Ser Lys Ser Glu Thr Thr Leu Glu Lys Leu Lys Gly  
 20 25 30

Glu Ile Ala His Leu Lys Thr Ser Val Asp Glu Ile Thr Ser Gly Lys  
 35 40 45

Gly Lys Leu Thr Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg  
 50 55 60

Val Leu Glu Ala Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys  
 65 70 75 80

Asp Lys Glu Ile Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser  
 85 90 95

Thr Thr Ala Leu Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu  
 100 105 110

Arg Arg Glu Gln Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu  
 115 120 125

Lys Gln Gln Leu Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser  
 130 135 140

Lys Thr Asn Thr Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe  
 145 150 155 160

Asn Ser Ser Ile Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp  
 165 170 175

Ala Leu Glu Lys Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu  
 180 185 190

Val Tyr Val Lys Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys  
 195 200 205

Thr Glu Thr Ala Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu  
 210 215 220

Ser Glu Gly Tyr Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu  
225 230 235 240

Leu Ala Ser Ala Lys Lys Asp Leu Glu Val Glu Arg Gln Thr Ile Thr  
245 250 255

Gln Leu Ser Phe Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr  
260 265 270

Gln Lys Glu Val His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg  
275 280 285

Ala Asp Val Gln His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile  
290 295 300

Gln Lys Leu Arg Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu  
305 310 315 320

Glu Lys Lys Arg Ser Glu Glu Leu Leu Ser Gln Val Gln Phe Leu Tyr  
325 330 335

Thr Ser Leu Leu Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu  
340 345 350

Glu Gln Gln Met Gln Ala Cys Thr Leu Asp Phe Glu Asn Glu Lys Leu  
355 360 365

Asp Arg Gln His Val Gln His Gln Leu Leu Val Ile Leu Lys Glu Leu  
370 375 380

Arg Lys Ala Arg Asn Gln Ile Thr Gln Leu Glu Ser Leu Lys Gln Leu  
385 390 395 400

His Glu Phe Ala Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr  
405 410 415

Glu Asn Arg Glu Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala  
420 425 430

Leu Asn Glu Ser Leu Val Glu Cys Pro Lys Cys Asn Ile Gln Tyr Pro  
435 440 445

Ala Thr Glu His Arg Asp Leu Leu Val His Val Glu Tyr Cys Ser Lys  
450 455 460

<210> 229

<211> 2635



<212> DNA  
<213> homo sapiens

<220>  
<221> CDS  
<222> (285)..(1679)

<400> 229  
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gaggggtggcg agggggcgcc aggaccgcga gcccggggc cggggcggtc cggaccgcga 120  
gggagggcag gtcagtgggc agatcgcgtc cgcgggattc aatctctgcc cgctctgata 180  
acagtccttt tccctggcgc tcaacttcgtg cctggcaccg ggctgggcgc ctcaagaccg 240  
ttgtctcttc gatcgcttct ttggacttgg cgaccatttc agag atg tct tcc aga 296  
Met Ser Ser Arg  
1  
agt acc aaa gat tta att aaa agt aag tgg gga tcg aag cct agt aac 344  
Ser Thr Lys Asp Leu Ile Lys Ser Lys Trp Gly Ser Lys Pro Ser Asn  
5 10 15 20  
tcc aaa tcc gaa act aca tta gaa aaa tta aag gga gaa att gca cac 392  
Ser Lys Ser Glu Thr Thr Leu Glu Lys Leu Lys Gly Glu Ile Ala His  
25 30 35  
tta aag aca tca gtg gat gaa atc aca agt ggg aaa gga aag ctg act 440  
Leu Lys Thr Ser Val Asp Glu Ile Thr Ser Gly Lys Gly Lys Leu Thr  
40 45 50  
gat aaa gag aga cac aga ctt ttg gag aaa att cga gtc ctt gag gct 488  
Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg Val Leu Glu Ala  
55 60 65  
gag aag gag aag aat gct tat caa ctc aca gag aag gac aaa gaa ata 536  
Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys Asp Lys Glu Ile  
70 75 80  
cag cga ctg aga gac caa ctg aag gcc aga tat agt act acc gca ttg 584  
Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser Thr Thr Ala Leu  
85 90 95 100  
ctt gaa cag ctg gaa gag aca acg aga gaa gga gaa agg agg gag cag 632  
Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu Arg Arg Glu Gln  
105 110 115  
gtg ttg aaa gcc tta tct gaa gag aaa gac gta ttg aaa caa cag ttg 680  
Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu Lys Gln Gln Leu  
120 125 130  
tct gct gca acc tca cga att gct gaa ctt gaa agc aaa acc aat aca 728  
Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser Lys Thr Asn Thr  
135 140 145  
ctc cgt tta tca cag act gtg gct cca aac tgc ttc aac tca tca ata 776  
Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe Asn Ser Ser Ile  
150 155 160

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cat ctg gaa gat gat agg cat aaa aca gag aag ata caa aaa ctc agg His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile Gln Lys Leu Arg 295 300 305	1208
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Leu Val Glu Cys Pro Lys Cys Asn Ile Gln Tyr Pro Ala Thr Glu His  
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Arg Asp Leu Leu Val His Val Glu Tyr Cys Ser Lys  
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Gly Lys Leu Thr Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg  
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Val Leu Glu Ala Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys  
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Asp Lys Glu Ile Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser  
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Thr Thr Ala Leu Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu  
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Arg Arg Glu Gln Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu  
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Lys Gln Gln Leu Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser  
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Lys Thr Asn Thr Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe  
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Asn Ser Ser Ile Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp  
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Ala Leu Glu Lys Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu  
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Val Tyr Val Lys Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys  
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Thr Glu Thr Ala Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu  
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Gln Lys Glu Val His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg  
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Ala Asp Val Gln His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile  
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Gln Lys Leu Arg Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu  
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Thr Ser Leu Leu Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu  
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Asp Arg Gln His Val Gln His Gln Leu Leu Val Ile Leu Lys Glu Leu  
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His Glu Phe Ala Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr  
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Val Asn Met Thr Pro Ser Glu Leu Met Asp Glu Ile Ile Ser Ile Arg	
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Val Tyr Asn Ser His Ser Leu Arg Ala Asp Cys Leu Met Gly Glu Phe	
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Lys Ile Asp Val Gly Phe Val Tyr Asp Glu Pro Gly His Ala Val Met	
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Arg Lys Trp Leu Leu Leu Asn Asp Pro Glu Asp Thr Ser Ser Gly Ser	
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Lys Gly Tyr Met Lys Val Ser Met Phe Val Leu Gly Thr Gly Asp Glu	
315 320 325	
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Pro Pro Pro Glu Arg Arg Asp Arg Asp Asn Asp Ser Asp Asp Val Glu	
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Ser Asn Leu Leu Leu Pro Ala Gly Ile Ala Leu Arg Trp Val Thr Phe	
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Phe Ser Gln Thr Val Lys Glu Ile Phe Gly Gly Asn Ala Asp Lys Lys	
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Asn Leu Val Asp Pro Phe Val Glu Val Ser Phe Ala Gly Lys Lys Val	
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Cys Thr Asn Ile Ile Glu Lys Asn Ala Asn Pro Glu Trp Asn Gln Val	
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Val Asn Leu Gln Ile Lys Phe Pro Ser Val Cys Glu Lys Ile Lys Leu	
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Thr Ile Tyr Asp Trp Asp Arg Leu Thr Lys Asn Asp Val Val Gly Thr	
445 450 455	
aca tat cta cac ctc tct aaa att gct gcc tct ggt ggg gaa gtg gaa	1504
Thr Tyr Leu His Leu Ser Lys Ile Ala Ala Ser Gly Gly Glu Val Glu	
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gat gag ctg aat act gga aag ggg gaa gga gtt gcc tac aga ggc agg Asp Glu Leu Asn Thr Gly Lys Gly Glu Gly Val Ala Tyr Arg Gly Arg 525 530 535			1696
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gcc aac gtc aca gtt ctc gat act cag atc cga aag ctg cgg tcc agg Ala Asn Val Thr Val Leu Asp Thr Gln Ile Arg Lys Leu Arg Ser Arg 715 720 725			2272



tct ctc tcc caa ata cat gag gcg gct gtg agg atg agg tcg gaa gcc Ser Leu Ser Gln Ile His Glu Ala Ala Val Arg Met Arg Ser Glu Ala 730 735 740	2320
aca gat gtg aag tcc aca ctg gca gaa att gag gac tgg ctt gat aaa Thr Asp Val Lys Ser Thr Leu Ala Glu Ile Glu Asp Trp Leu Asp Lys 745 750 755 760	2368
tta atg cag ctg act gaa gag cca cag aac agc atg cct gac atc atc Leu Met Gln Leu Thr Glu Glu Pro Gln Asn Ser Met Pro Asp Ile Ile 765 770 775	2416
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Phe Leu Gly Arg Ser	Ile Phe Ser Pro Val	Val Lys Leu Asn Ser	
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Gly Asp Lys Ala Cys	Gly Asp Val Leu Val	Thr Ala Glu Leu Ile	
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Leu Arg Gly Lys Asp	Gly Ser Asn Leu Pro	Ile Leu Pro Pro Gln	
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Arg Ala Pro Asn Leu	Tyr Met Val Pro Gln	Gly Ile Arg Pro Val	
1290	1295	1300	
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Val Gln Leu Thr Ala	Ile Glu Ile Leu Ala	Trp Gly Leu Arg Asn	
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Met Lys Asn Phe Gln	Met Ala Ser Ile Thr	Ser Pro Ser Leu Val	
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Val Glu Cys Gly Gly	Glu Arg Val Glu Ser	Val Val Ile Lys Asn	
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Lys Val Ile Asp His	Arg Gln Phe Gly Arg	Lys Pro Val Val Gly	
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Gln Cys Thr Ile Glu	Arg Leu Asp Arg Phe	Arg Cys Asp Pro Tyr	
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Ser Ala Pro Pro Cys	Arg Asp Ile Val Ile	Glu Met Glu Asp Thr	

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Lys Cys Gly Gln Tyr	Ile Gln Lys Gly Tyr	Ser Lys Leu Lys Ile	
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Tyr Asn Cys Glu Leu	Glu Asn Val Ala Glu	Phe Glu Gly Leu Thr	
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Arg Ile Tyr Ile Val	Arg Gly Leu Glu Leu	Gln Pro Gln Asp Asn	
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Asn Gly Leu Cys Asp	Pro Tyr Ile Lys Ile	Thr Leu Gly Lys Lys	
1575	1580	1585	
gtc att gaa gac cga	gat cac tac att ccc	aac act ctc aac cca	4888
Val Ile Glu Asp Arg	Asp His Tyr Ile Pro	Asn Thr Leu Asn Pro	
1590	1595	1600	
gtc ttt ggc agg atg	tac gaa ctg agc tgc	tac tta cct caa gaa	4933
Val Phe Gly Arg Met	Tyr Glu Leu Ser Cys	Tyr Leu Pro Gln Glu	
1605	1610	1615	
aaa gac ctg aaa att	tct gtc tat gat tat	gac acc ttt acc cgg	4978
Lys Asp Leu Lys Ile	Ser Val Tyr Asp Tyr	Asp Thr Phe Thr Arg	
1620	1625	1630	
gat gaa aaa gta gga	gaa aca att att gat	ctg gaa aac cga ttc	5023
Asp Glu Lys Val Gly	Glu Thr Ile Ile Asp	Leu Glu Asn Arg Phe	
1635	1640	1645	
ctt tcc cgc ttt ggg	tcc cac tgc ggc ata	cca gag gag tac tgt	5068
Leu Ser Arg Phe Gly	Ser His Cys Gly Ile	Pro Glu Glu Tyr Cys	
1650	1655	1660	

gtt tct gga gtc aat	acc tgg cga gat caa	ctg aga cca aca cag	5113
Val Ser Gly Val Asn	Thr Trp Arg Asp Gln	Leu Arg Pro Thr Gln	
1665	1670	1675	
ctg ctt caa aat gtc	gcc aga ttc aaa ggc	ttc cca caa ccc atc	5158
Leu Leu Gln Asn Val	Ala Arg Phe Lys Gly	Phe Pro Gln Pro Ile	
1680	1685	1690	
ctt tcc gaa gat ggg	agt aga atc aga tat	gga gga cga gac tac	5203
Leu Ser Glu Asp Gly	Ser Arg Ile Arg Tyr	Gly Gly Arg Asp Tyr	
1695	1700	1705	
agc ttg gat gaa ttt	gaa gcc aac aaa atc	ctg cac cag cac ctc	5248
Ser Leu Asp Glu Phe	Glu Ala Asn Lys Ile	Leu His Gln His Leu	
1710	1715	1720	
ggg gcc cct gaa gag	cgg ctt gct ctt cac	atc ctc agg act cag	5293
Gly Ala Pro Glu Glu	Arg Leu Ala Leu His	Ile Leu Arg Thr Gln	
1725	1730	1735	
ggg ctg gtc cct gag	cac gtg gaa aca agg	act ttg cac agc acc	5338
Gly Leu Val Pro Glu	His Val Glu Thr Arg	Thr Leu His Ser Thr	
1740	1745	1750	
ttc cag ccc aac att	toc cag gga aaa ctt	cag atg tgg gtg gat	5383
Phe Gln Pro Asn Ile	Ser Gln Gly Lys Leu	Gln Met Trp Val Asp	
1755	1760	1765	
gtt ttc ccc aag agt	ttg ggg cca cca ggc	cct cct ttc aac atc	5428
Val Phe Pro Lys Ser	Leu Gly Pro Pro Gly	Pro Pro Phe Asn Ile	
1770	1775	1780	
aca ccc cgg aaa gcc	aag aaa tac tac ctg	cgt gtg atc atc tgg	5473
Thr Pro Arg Lys Ala	Lys Lys Tyr Tyr Leu	Arg Val Ile Ile Trp	
1785	1790	1795	
aac acc aag gac gtt	atc ttg gac gag aaa	agc atc aca gga gag	5518
Asn Thr Lys Asp Val	Ile Leu Asp Glu Lys	Ser Ile Thr Gly Glu	
1800	1805	1810	
gaa atg agt gac atc	tac gtc aaa ggc tgg	att cct ggc aat gaa	5563
Glu Met Ser Asp Ile	Tyr Val Lys Gly Trp	Ile Pro Gly Asn Glu	
1815	1820	1825	
gaa aac aaa cag aaa	aca gat gtc cat tac	aga tct ttg gat ggt	5608
Glu Asn Lys Gln Lys	Thr Asp Val His Tyr	Arg Ser Leu Asp Gly	
1830	1835	1840	
gaa ggg aat ttt aac	tgg cga ttt gtt ttc	cgg ttt gac tac ctt	5653
Glu Gly Asn Phe Asn	Trp Arg Phe Val Phe	Pro Phe Asp Tyr Leu	
1845	1850	1855	
cca gcc gaa caa ctc	tgt atc gtt gcg aaa	aaa gag cat ttc tgg	5698
Pro Ala Glu Gln Leu	Cys Ile Val Ala Lys	Lys Glu His Phe Trp	
1860	1865	1870	
agt att gac caa acg	gaa ttt cga atc cca	ccc agg ctg atc att	5743
Ser Ile Asp Gln Thr	Glu Phe Arg Ile Pro	Pro Arg Leu Ile Ile	
1875	1880	1885	

cag ata tgg gac aat	gac aag ttt tct ctg	gat gac tac ttg ggt	5788
Gln Ile Trp Asp Asn	Asp Lys Phe Ser Leu	Asp Asp Tyr Leu Gly	
1890	1895	1900	
ttc cta gaa ctt gac	ttg cgt cac acg atc	att cct gca aaa tca	5833
Phe Leu Glu Leu Asp	Leu Arg His Thr Ile	Ile Pro Ala Lys Ser	
1905	1910	1915	
cca gag aaa tgc agg	ttg gac atg att ccg	gac ctc aaa gcc atg	5878
Pro Glu Lys Cys Arg	Leu Asp Met Ile Pro	Asp Leu Lys Ala Met	
1920	1925	1930	
aac ccc ctt aaa gcc	aag aca gcc tcc ctc	ttt gag cag aag tcc	5923
Asn Pro Leu Lys Ala	Lys Thr Ala Ser Leu	Phe Glu Gln Lys Ser	
1935	1940	1945	
atg aaa gga tgg tgg	cca tgc tac gca gag	aaa gat ggc gcc cgc	5968
Met Lys Gly Trp Trp	Pro Cys Tyr Ala Glu	Lys Asp Gly Ala Arg	
1950	1955	1960	
gta atg gct ggg aaa	gtg gag atg aca ttg	gaa atc ctc aac gag	6013
Val Met Ala Gly Lys	Val Glu Met Thr Leu	Glu Ile Leu Asn Glu	
1965	1970	1975	
aag gag gcc gac gag	agg cca gcc ggg aag	ggg cgg gac gaa ccc	6058
Lys Glu Ala Asp Glu	Arg Pro Ala Gly Lys	Gly Arg Asp Glu Pro	
1980	1985	1990	
aac atg aac ccc aag	ctg gac tta cca aat	cga cca gaa acc tcc	6103
Asn Met Asn Pro Lys	Leu Asp Leu Pro Asn	Arg Pro Glu Thr Ser	
1995	2000	2005	
ttc ctc tgg ttc acc	aac cca tgc aag acc	atg aag ttc atc gtg	6148
Phe Leu Trp Phe Thr	Asn Pro Cys Lys Thr	Met Lys Phe Ile Val	
2010	2015	2020	
tgg cgc cgc ttt aag	ttg gtc atc atc ggc	ttg ctg ttc ctg ctt	6193
Trp Arg Arg Phe Lys	Trp Val Ile Ile Gly	Leu Leu Phe Leu Leu	
2025	2030	2035	
atc ctg ctg ctc ttc	gtg gcc gtg ctc ctc	tac tct ttg ccg aac	6238
Ile Leu Leu Leu Phe	Val Ala Val Leu Leu	Tyr Ser Leu Pro Asn	
2040	2045	2050	
tat ttg tca atg aag	att gta aag cca aat	gtg taa caaaggcaaa	6284
Tyr Leu Ser Met Lys	Ile Val Lys Pro Asn	Val	
2055	2060		
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35 40 45

Ile Leu Glu Phe Asp Leu Arg Gly Ile Pro Leu Asp Phe Ser Ser Ser  
50 55 60

Leu Gly Ile Ile Val Lys Asp Phe Glu Thr Ile Gly Gln Asn Lys Leu  
65 70 75 80

Ile Gly Thr Ala Thr Val Ala Leu Lys Asp Leu Thr Gly Asp Gln Ser  
85 90 95

Arg Ser Leu Pro Tyr Lys Leu Ile Ser Leu Leu Asn Glu Lys Gly Gln  
100 105 110

Asp Thr Gly Ala Thr Ile Asp Leu Val Ile Gly Tyr Asp Pro Pro Ser  
115 120 125

Ala Pro His Pro Asn Asp Leu Ser Gly Pro Ser Val Pro Gly Met Gly  
130 135 140

Gly Asp Gly Glu Glu Asp Glu Gly Asp Glu Asp Arg Leu Asp Asn Ala  
145 150 155 160

Val Arg Gly Pro Gly Pro Lys Gly Pro Val Gly Thr Val Ser Glu Ala  
165 170 175

Gln Leu Ala Arg Arg Leu Thr Lys Val Lys Asn Ser Arg Arg Met Leu  
180 185 190

Ser Asn Lys Pro Gln Asp Phe Gln Ile Arg Val Arg Val Ile Glu Gly  
 195 200 205

Arg Gln Leu Ser Gly Asn Asn Ile Arg Pro Val Val Lys Val His Val  
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Cys Gly Gln Thr His Arg Thr Arg Ile Lys Arg Gly Asn Asn Pro Phe  
 225 230 235 240

Phe Asp Glu Leu Phe Phe Tyr Asn Val Asn Met Thr Pro Ser Glu Leu  
 245 250 255

Met Asp Glu Ile Ile Ser Ile Arg Val Tyr Asn Ser His Ser Leu Arg  
 260 265 270

Ala Asp Cys Leu Met Gly Glu Phe Lys Ile Asp Val Gly Phe Val Tyr  
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Asp Glu Pro Gly His Ala Val Met Arg Lys Trp Leu Leu Leu Asn Asp  
 290 295 300

Pro Glu Asp Thr Ser Ser Gly Ser Lys Gly Tyr Met Lys Val Ser Met  
 305 310 315 320

Phe Val Leu Gly Thr Gly Asp Glu Pro Pro Pro Glu Arg Arg Asp Arg  
 325 330 335

Asp Asn Asp Ser Asp Asp Val Glu Ser Asn Leu Leu Leu Pro Ala Gly  
 340 345 350

Ile Ala Leu Arg Trp Val Thr Phe Leu Leu Lys Ile Tyr Arg Ala Glu  
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Asp Ile Pro Gln Met Asp Asp Ala Phe Ser Gln Thr Val Lys Glu Ile  
 370 375 380

Phe Gly Gly Asn Ala Asp Lys Lys Asn Leu Val Asp Pro Phe Val Glu

Val Ser Phe Ala Gly Lys Lys Val Cys Thr Asn Ile Ile Glu Lys Asn  
 405 410 415

Ala Asn Pro Glu Trp Asn Gln Val Val Asn Leu Gln Ile Lys Phe Pro  
 420 425 430



Ser Val Cys Glu Lys Ile Lys Leu Thr Ile Tyr Asp Trp Asp Arg Leu  
435 440 445

Thr Lys Asn Asp Val Val Gly Thr Thr Tyr Leu His Leu Ser Lys Ile  
450 455 460

Ala Ala Ser Gly Gly Glu Val Glu Asp Phe Ser Ser Ser Gly Thr Gly  
465 470 475 480

Ala Ala Ser Tyr Thr Val Asn Thr Gly Glu Thr Glu Val Gly Phe Val  
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Pro Thr Phe Gly Pro Cys Tyr Leu Asn Leu Tyr Gly Ser Pro Arg Glu  
500 505 510

Tyr Thr Gly Phe Pro Asp Pro Tyr Asp Glu Leu Asn Thr Gly Lys Gly  
515 520 525

Glu Gly Val Ala Tyr Arg Gly Arg Ile Leu Val Glu Leu Ala Thr Phe  
530 535 540

Leu Glu Lys Thr Pro Pro Asp Lys Lys Leu Glu Pro Ile Ser Asn Asp  
545 550 555 560

Asp Leu Leu Val Val Glu Lys Tyr Gln Arg Arg Arg Lys Tyr Ser Leu  
565 570 575

Ser Ala Val Phe His Ser Ala Thr Met Leu Gln Asp Val Gly Glu Ala  
580 585 590

Ile Gln Phe Glu Val Ser Ile Gly Asn Tyr Gly Asn Lys Phe Asp Thr  
595 600 605

Thr Cys Lys Pro Leu Ala Ser Thr Thr Gln Tyr Ser Arg Ala Val Phe  
610 615 620

Asp Gly Asn Tyr Tyr Tyr Tyr Leu Pro Trp Ala His Thr Lys Pro Val  
625 630 635 640

Val Thr Leu Thr Ser Tyr Trp Glu Asp Ile Ser His Arg Leu Asp Ala  
645 650 655

Val Asn Thr Leu Leu Ala Met Ala Glu Arg Leu Gln Thr Asn Ile Glu  
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Ala Leu Lys Ser Gly Ile Gln Gly Lys Ile Pro Ala Asn Gln Leu Ala

675

680

685

Glu Leu Trp Leu Lys Leu Ile Asp Glu Val Ile Glu Asp Thr Arg Tyr  
690 695 700

Thr Leu Pro Leu Thr Glu Gly Lys Ala Asn Val Thr Val Leu Asp Thr  
705 710 715 720

Gln Ile Arg Lys Leu Arg Ser Arg Ser Leu Ser Gln Ile His Glu Ala  
725 730 735

Ala Val Arg Met Arg Ser Glu Ala Thr Asp Val Lys Ser Thr Leu Ala  
740 745 750

Glu Ile Glu Asp Trp Leu Asp Lys Leu Met Gln Leu Thr Glu Glu Pro  
755 760 765

Gln Asn Ser Met Pro Asp Ile Ile Ile Trp Met Ile Arg Gly Glu Lys  
770 775 780

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785 790 795 800

Ser Gly Glu Asn Ala Ser Gly Lys Tyr Cys Gly Lys Thr Gln Thr Ile  
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Gly Arg His Lys Phe Ser Asp Val Thr Gly Lys Ile Lys Leu Lys Arg  
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Trp Glu Tyr Gly Ile Thr Ile Pro Pro Asp His Lys Pro Lys Ser Trp  
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Val Ala Ala Glu Lys Met Tyr His Thr His Arg Arg Arg Arg Leu  
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Ala Ser Leu Ile Gly Trp Lys Phe His Trp Lys Gln Arg Ser Ser  
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Asp Thr Phe Arg Arg Arg Arg Trp Arg Arg Lys Met Ala Pro Ser  
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Gly Ala Asp Thr Thr Glu Asp Gly Asp Glu Lys Ser Leu Glu Lys  
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Gln Lys His Ser Ala Thr Thr Val Phe Gly Ala Asn Thr Pro Ile  
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Val Ser Cys Asn Phe Asp Arg Val Tyr Ile Tyr His Leu Arg Cys  
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Tyr Val Tyr Gln Ala Arg Asn Leu Leu Ala Leu Asp Lys Asp Ser  
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Phe Ser Asp Pro Tyr Ala His Ile Cys Phe Leu His Arg Ser Lys  
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 Thr Thr Glu Ile Ile His Ser Thr Leu Asn Pro Thr Trp Asp Gln  
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 Pro Val Val Lys Leu Asn Ser Glu Met Asp Ile Thr Pro Lys Leu  
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 Leu Val Thr Ala Glu Leu Ile Leu Arg Gly Lys Asp Gly Ser Asn  
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 Glu Ser Val Val Ile Lys Asn Leu Lys Lys Thr Pro Asn Phe Pro  
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 Ser Ser Val Leu Phe Met Lys Val Phe Leu Pro Lys Glu Glu Leu  
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 Tyr Met Pro Pro Leu Val Ile Lys Val Ile Asp His Arg Gln Phe  
 1370 1375 1380  
 Gly Arg Lys Pro Val Val Gly Gln Cys Thr Ile Glu Arg Leu Asp

176

Asp Tyr Asp Thr Phe Thr Arg Asp Glu Lys Val Gly Glu Thr Ile  
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Ile Asp Leu Glu Asn Arg Phe Leu Ser Arg Phe Gly Ser His Cys  
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Gly Ile Pro Glu Glu Tyr Cys Val Ser Gly Val Asn Thr Trp Arg  
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Asp Gln Leu Arg Pro Thr Gln Leu Leu Gln Asn Val Ala Arg Phe  
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Lys Gly Phe Pro Gln Pro Ile Leu Ser Glu Asp Gly Ser Arg Ile  
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Arg Tyr Gly Gly Arg Asp Tyr Ser Leu Asp Glu Phe Glu Ala Asn  
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Lys Ile Leu His Gln His Leu Gly Ala Pro Glu Glu Arg Leu Ala  
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Leu His Ile Leu Arg Thr Gln Gly Leu Val Pro Glu His Val Glu  
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Thr Arg Thr Leu His Ser Thr Phe Gln Pro Asn Ile Ser Gln Gly  
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Lys Leu Gln Met Trp Val Asp Val Phe Pro Lys Ser Leu Gly Pro  
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Tyr Leu Arg Val Ile Ile Trp Asn Thr Lys Asp Val Ile Leu Asp  
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Glu Lys Ser Ile Thr Gly Glu Glu Met Ser Asp Ile Tyr Val Lys  
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Gly Trp Ile Pro Gly Asn Glu Glu Asn Lys Gln Lys Thr Asp Val  
 1820 1825 1830

His Tyr Arg Ser Leu Asp Gly Glu Gly Asn Phe Asn Trp Arg Phe  
 1835 1840 1845

Val Phe Pro Phe Asp Tyr Leu Pro Ala Glu Gln Leu Cys Ile Val

1850	1855	1860
Ala Lys Lys Glu His Phe Trp	Ser Ile Asp Gln Thr	Glu Phe Arg
1865	1870	1875
Ile Pro Pro Arg Leu Ile Ile	Gln Ile Trp Asp Asn	Asp Lys Phe
1880	1885	1890
Ser Leu Asp Asp Tyr Leu Gly	Phe Leu Glu Leu Asp	Leu Arg His
1895	1900	1905
Thr Ile Ile Pro Ala Lys Ser	Pro Glu Lys Cys Arg	Leu Asp Met
1910	1915	1920
Ile Pro Asp Leu Lys Ala Met	Asn Pro Leu Lys Ala	Lys Thr Ala
1925	1930	1935
Ser Leu Phe Glu Gln Lys Ser	Met Lys Gly Trp Trp	Pro Cys Tyr
1940	1945	1950
Ala Glu Lys Asp Gly Ala Arg	Val Met Ala Gly Lys	Val Glu Met
1955	1960	1965
Thr Leu Glu Ile Leu Asn Glu	Lys Glu Ala Asp Glu	Arg Pro Ala
1970	1975	1980
Gly Lys Gly Arg Asp Glu Pro	Asn Met Asn Pro Lys	Leu Asp Leu
1985	1990	1995
Pro Asn Arg Pro Glu Thr Ser	Phe Leu Trp Phe Thr	Asn Pro Cys
2000	2005	2010
Lys Thr Met Lys Phe Ile Val	Trp Arg Arg Phe Lys	Trp Val Ile
2015	2020	2025
Ile Gly Leu Leu Phe Leu Leu	Ile Leu Leu Leu Phe	Val Ala Val
2030	2035	2040
Leu Leu Tyr Ser Leu Pro Asn	Tyr Leu Ser Met Lys	Ile Val Lys
2045	2050	2055
Pro Asn Val		
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&lt;212&gt; RNA

&lt;213&gt; Artificial Sequence

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&lt;223&gt; RNAi molecule

&lt;400&gt; 245

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&lt;223&gt; RNAi molecule

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&lt;211&gt; 27

&lt;212&gt; RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; RNAi molecule

&lt;400&gt; 247

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&lt;210&gt; 248

&lt;211&gt; 27

&lt;212&gt; RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; RNAi molecule

&lt;400&gt; 248

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27

&lt;210&gt; 249

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&lt;212&gt; RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; RNAi molecule

&lt;400&gt; 249

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27

&lt;210&gt; 250

&lt;211&gt; 27

&lt;212&gt; RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; RNAi molecule

&lt;400&gt; 250

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27

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&lt;211&gt; 27

&lt;212&gt; RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; RNAi molecule

&lt;400&gt; 251

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&lt;212&gt; RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; RNAi molecule

&lt;400&gt; 252

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